SEQUENCE LISTING

<110> BLUMENFELD, Marta
BOUGUELERET, Lydie
CHUMAKOV, Ilya
COHEN, Daniel
ESSIOUX, Laurent

<120> Genes, proteins and biallelic markers related to central nervous system disease.

<130> 50.US3.PCT

<140> US 09/807,506
<141> 2001-04-13

<150> US 60/106,457
<151> 1998-10-30

<150> US 60/103,955
<151> 1998-10-13

<160> 71

<170> Patent.pm

<210> 1
<211> 5222
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1076..3075
<223> 5' regulatory region

<220>
<221> exon
<222> 3076..4643
<223> exon 1

<220>
<221> allele
<222> 4872
<223> 8-58-301 : polymorphic base C or T

<220>
<221> allele
<222> 3606
<223> insertion of AGAG in SEQID4

<220>
<221> primer_bind
<222> 4572..4587
<223> 8-58.pu

<220>

<221> primer_bind
<222> 4990..5005
<223> 8-58.rp complement

<220>
<221> misc_binding
<222> 4849..4895
<223> 8-58-301.probe

<220>
<221> primer_bind
<222> 4853..4871
<223> 8-58-301.mis

<220>
<221> primer_bind
<222> 4873..4891
<223> 8-58-301.mis complement

<220>
<221> misc_feature
<222> 148,686,902,1258,1322,2440,2794,2852,3018..3023,3052..3053,3064
3067,3428..3429,3489,3545,5131,5182
<223> n=a, g, c or t

<400> 1
caatatacag gtcacacaca acacagccca cttatctgtc agtagtccta ccagtgccct 60
gggctccttc aaggtcccaa gtccttgaaa tttgctgtcc ttctgaattg tccttttctc 120
ctccctagaa gacttctttc tgctcccntt aaatgtcccc aattcctatc tatccctagt 180
ccctcttaaa atccaactgg agtttactgc tctactctga agtctcaaaa catgctaatc 240
ttcacagatt accttgtatt gtaattgttg gcctagttag tattatctgc cccttgacta 300
agcttcaaga ggccagactt ggtcttttat ctgtcttcca acagttcatt ctagaaccaa 360
cacacaacaa acaaaagtca aattggttct caacagttta ctttcagtgg gcttgcgtcc 420
ttaaaattgt cttttataaa aatatcctaa ttcatgagaa acattagagg aaggcaaggc 480
ccagcttact taaaaataat taactatagt ctgttacata aagtaaaaat agattaaaca 540
ctattatttt aatgcagtat ataagacttt tactaagtat cactgaacta ccttctgaga 600
catgattttt actagatctg aatagtaata agataagtca cagagtcttc ttttgcttcg 660
gttccttgtt tgataattat gaaccnttta aatttatatt gtttatttta tttcccctag 720
ttttcgttct ctttctgatt taatcacaca tgcagagtaa gacattggat gctaataatc 780
tcagccacca ttaaaatgtt tgtgtctgat taaaattaat gcattattga agggaaatat 840
attattatct aataagtgtg gatgtgtatt ctatcatact tcaatccttc gaaaatgctg 900
gnactagtga atatcacaaa acaggaaatt agtaatacaa aataaaaatg ttaggaagat 960
gctgtaaaat gaaaatactg attatatctg ggtgttgata tcaccatgac tttttaaatt 1020
gctcttctga ttttttacacc ttttttacaa tgcacaaact gtacttgtat aataatagtt 1080
atgtcagcga gaatgtatgc actcgtattt agttaagaaa tattgtggca tgtacagtac 1140
agtcctgatt aataaacaat ctggttaata aataataatt ttgtctgtat tatgaggaaa 1200
aactgacatt actcagaaat tcaacacact gaaatcgaaa gtactagaat gatctacntt 1260
acacaaatcg tcttttaaaa cactacatga cacttgagta aaccagccat caaacaggac 1320
gncggctttt ggatgatcat tacctatagt tggtaagaac tgaaaatttt taggggtaaa 1380
atttagtgta tacagtacct tattatgcag cagaagaggc tagtaggtcg aatcctgccc 1440
aagaggtttt gcaattttct ctttaaaaaa cacctacttc tcccgcatcc ccaacaccca 1500
cagcgctcct taaaggaaaa tggatacgga tgccccatcc ctttggtttc tcaatgcatt 1560
ttacttagaa agaggtcacc tagtaagacc catgtggtga atgtgcaccc gggcggggca 1620
tgagggtcct tggaaagcac cgcagagagg gcgacaccgc aaaccgctgt cccacgcgac 1680
ccccggggcg agccggggca gcgctgcact cggtgcgcac cggcagcgtc tggcacccac 1740
gccacctgct gctcccgcgg gtctggcagg ggcaaggggc ggagtgggca ggatcttcag 1800
atcaaaggag accgatgctt gcccacggca tccagcgtag gagccggaat cgaggtgacc 1860
ccagattttc ccagagtgtc tgtctccttt cccttctcag aactccgaga gccaacgcta 1920

aggggcacca gaggctcaga ctgcggcggc gactcgcagg cacccagctc gcccgcggct 1980
gcggaggtcc tcggaggagc ccacccggga gggggtctgg acgcaggcag cgggggcaga 2040
gggagggtcg aagccgctcc agagggtcca ggtccgagga ggagccctcg gagacgcgga 2100
cggtgcgcgc ggagggcagg gctaggcagt gaccccgggt ggcacagggc ttactgtttc 2160
ttcctaagac tctatgaggc cacttctaat cgtttacttt agaataggaa agaaaacata 2220
gacaaatggg tggctgtcac ccaggcagct acacggtcga tgcaggtgca caggcgtgcg 2280
cgccattctc ccgtgtcaca cagcaggacg gaataactgc acgcactggg agcgatggat 2340
ctcgcggtcc gggatccgag acgcattcag agaccaaatg tcacctcatc cctcctctag 2400
ccaattcgag cttcctccgc ggacccccac cttccatccn gaagtggctc ggtccttagt 2460
tgagaggact ctgcccagac cctcgcacca gtagagacct ctgcccgggc gcctgcaact 2520
cggacgcttc ccggagccag agcgtgcggg cggcgcggcc gcgaggagcc tcaccggcca 2580
tgccgtccgc agtctgactt ttatttttct cttcagtgat taaaacaaaa tatcgtggac 2640
agggggacag aaaggaaaga gcaggcgcct gagcccgggg agccgggcgg gggccccccgg 2700
gccccgcggc cccgccgccg cccgcccccg cgcgccttct ccctcctccc gggccgagcc 2760
ggcgccactg cgccaggatg gagcgagctc ggcngcggga ggagatgacg caaaagccag 2820
cgctcccccc aaaaaagtgt ttctccagga cngaagatgg cggcaactta gcccgcggac 2880
tgaagatgac tgtggctctc gggaggccca gcccaggcga ttcggcccgg agctccgcgg 2940
gaggcggcgt cagcagtcgg agccccggcg gcggcgcccg cgggcggccc tgcggcagcg 3000
gcggcggcgg cggcggcnnn nnnagcactt agagcgcggg gtgggggggtg gnnggggaggg 3060
agcngcnccg ccggaggcag cccaggctcc ggactctggg agagccagcg cggagcagga 3120
gcgggaggcg gaggagaaga agaaggagaa ggaaaggaag gaggaggaag aggaggagaa 3180
gaagaggagg aggaggagga ggaggggagg cgctccgggc gccgtcagtg ggcagcggag 3240
gcgcggcatg cccctggcag gggagagcgg gctgggctcc gcggggccat ggggacccgc 3300
gcgctgacaa tgcctgggtg accggagccg cgccagccac cctgtcacct ccaccatcgc 3360
cccctgcacc cagcctcgcc gccggccacc agcaccagcc tcctccgtct ctctctctct 3420
ctctctcnnc attattgttt cccactctac agaggatggg gtcggctgat gattaggaag 3480
caagtcagnc cttccttcaa agcctggtaa tatttatgta ggcaaaagag acagagagag 3540
ataanagaga gggagaggga gagagagaga gaggagagag ggagagggga agagagagaa 3600
agagaggaga gagaagaaac gggaggaggg gataaggaaa ttaaaccctt taagtcaatg 3660
catattgtgg tgacaccggc acaggcgccc tcacggtgga gtcggccagg gctgtgcgtt 3720
cccaaaatat gaccaggggt gcttggatgt gtcggcagta tgacgacggc ttaaaaatct 3780
ggttggcagc accccgagag aacgagaaac cgttcatcga ttccgagagg gctcagaaat 3840
ggcgactgtc tctggcatct ctcttgtttt tcacagtcct gctctctgat cacttgtggt 3900
tctgcgccga ggccaagctg acccgggccc gggacaagga gcaccagcag cagcagcggc 3960
agcagcagca gcagcagcag cagcagaggc agcggcagca gcagcagcag cagcggcggc 4020
agcaggagcc ctcctggccc gcgctcctgg cgagcatggg ggagtcctcg cccgccgccc 4080
aggcacacag actcctctcc gcctcctcgt cccccaccct gccccccctcc ccgggagacg 4140
gcggcggcgg cggcggcaag ggcaaccgag gcaaagacga ccggggcaag gctctttttc 4200
taggaaactc tgccaagccc gtgtggcgcc tggagacttg ttacccccag ggcgcgtcct 4260
cgggccagtg cttcacggtg gagaatgcgg acgcggtgtg cgccaggaac tggagtcggg 4320
gggcggccgg gggggacggg caggaggtga ggagcaagca tcccactccg ctctggaact 4380
tgtcggattt ttacctttcg ttttgtaatt cctacacact ttgggagttg ttctcggggt 4440
tgtccagtcc caacactttg aactgcagtc tggatgtggt gctcaaggaa ggcggcgaga 4500
tgaccacttg caggcagtgc gtcgaggctt accaggacta tgaccaccat gctcaggaga 4560
aatacgaaga gtttgaaagc gtgctccaca aatatttaca gtcggaggag tactcggtga 4620
aatcctgtcc tgaagactgt aaggtaggaa ccctcggggg tttccccctt tcctgcactt 4680
tcctatctct gcttggttgg ggtgtcttct caagtttatt attattattt tttggctatg 4740
gttttgttac tttgtgtttt ctgcggttat taagagcttg gcttgctgtt tgagatgaga 4800
atacctggtg gattgctggt ggactgactg atgccttctt ctgggagtcc ttggaagatc 4860
agggaagtcc cyggttatct gagataatca agctggcact ttaactgttt cttacattca 4920
tgcagttggc tcaaactctg ttacatcttt taagaaaagg aagttgaaaa agtcttgtca 4980
ggaaaatagc aatgagactg cacactgatg ctcacaggta aagtcagaag agttcgagac 5040
aggcatgtgt ggtttgcaat atagatctgc acacaggaac gctctcatag tgacatcatt 5100
aagttggttg agcaagagaa gtggttgtag nttgtttcgg tagttaaaaa gaattacctg 5160
tttttacagg ggtaattctg gntgttcaga aaagtctggg ggcctacctg aggatattta 5220
ct 5222

<210> 2

<211> 21278
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> 16158..16329
<223> exon 2

<220>
<221> allele
<222> 3262
<223> 99-16063-218 : polymorphic base A or G

<220>
<221> allele
<222> 6231
<223> 99-16073-282 : polymorphic base A or G

<220>
<221> allele
<222> 9871
<223> 99-16074-266 : polymorphic base C or T

<220>
<221> allele
<222> 14968
<223> 99-13817-215 : polymorphic base C or T

<220>
<221> allele
<222> 20259
<223> 99-16066-123 : polymorphic base C or T

<220>
<221> primer_bind
<222> 3045..3062
<223> 99-16063.pu

<220>
<221> primer_bind
<222> 3547..3565
<223> 99-16063.rp complement

<220>
<221> primer_bind
<222> 6058..6076
<223> 99-16073.rp

<220>
<221> primer_bind
<222> 6493..6512
<223> 99-16073.pu complement

<220>
<221> primer_bind
<222> 9661..9678
<223> 99-16074.rp

<220>
<221> primer_bind
<222> 10119..10136
<223> 99-16074.pu complement

<220>
<221> primer_bind
<222> 14754..14774
<223> 99-13817.pu

<220>
<221> primer_bind
<222> 15183..15203
<223> 99-13817.rp complement

<220>
<221> primer_bind
<222> 20137..20155
<223> 99-16066.pu

<220>
<221> primer_bind
<222> 20569..20588
<223> 99-16066.rp complement

<220>
<221> misc_binding
<222> 3239..3285
<223> 99-16063-218.probe

<220>
<221> misc_binding
<222> 6208..6254
<223> 99-16073-282.probe

<220>
<221> misc_binding
<222> 9848..9894
<223> 99-16074-266.probe

<220>
<221> misc_binding
<222> 14945..14991
<223> 99-13817-215.probe

<220>
<221> misc_binding
<222> 20236..20282
<223> 99-16066-123.probe

<220>
<221> primer_bind
<222> 3243..3261
<223> 99-16063-218.mis

<220>
<221> primer_bind

<222> 3263..3281
<223> 99-16063-218.mis complement

<220>
<221> primer_bind
<222> 6212..6230
<223> 99-16073-282.mis

<220>
<221> primer_bind
<222> 6232..6250
<223> 99-16073-282.mis complement

<220>
<221> primer_bind
<222> 9852..9870
<223> 99-16074-266.mis

<220>
<221> primer_bind
<222> 9872..9890
<223> 99-16074-266.mis complement

<220>
<221> primer_bind
<222> 14949..14967
<223> 99-13817-215.mis

<220>
<221> primer_bind
<222> 14969..14987
<223> 99-13817-215.mis complement

<220>
<221> primer_bind
<222> 20240..20258
<223> 99-16066-123.mis

<220>
<221> primer_bind
<222> 20260..20278
<223> 99-16066-123.mis complement

<220>
<221> misc_feature
<222> 285,982,2264,2273,2823,11227,11232,13663,13681,13842..13843
16849..16851,17022,17091,18127,20930,20962,20994,21207
<223> n=a, g, c or t

<400> 2
gggcgcatca gttctgggag atgaactctg gcttcacttc agtcagggac ttaaactttc 60
tgggcctcgt attttcaaac ccatggaata gaggaaaaat attactgtct acctcagagg 120
tttgtgtaag aattaaatga gttactacat gtaagacctt tatctagttg ctggcatgca 180
gtgagtgcta tgccagcatc agtagttatc ttctgctttt gtaaatatgt tgcattggtg 240
agatttgaaa tcaccgtttc aaattcacta tgatcattta tattngctgt gcgttgatag 300
tggttataaa aagtcagaaa cccgatgcta agtatgtttt acattatagt ctatgaaatt 360
cgagcaacag gattttatgt tttgtcatgt actcattttg ttccacagtg aataagaatc 420
tgtttcaaat gaacttttac atttatacca tgtgaaagaa acagattatt ggataatttt 480

tcattgtaaa agaaacaatt tccatctaag catttacaca ttctaataaa tgtatagtta 540
acgttatttt gtgcttacgc tgaaaaatgt aaaagatatt ttctggcttg acctgatttt 600
aaataatagt gagtatctta aattctaagg aataaaataa aaccgtattt ttgccggggt 660
tttctgaccg cctctttcca taacatacaa ttggcttccc tttctgtctg ccttgtccaa 720
ggtcttcatc caatgcagcc tgctctctgg aggctctgct gtttaggtag tggtgtgtgt 780
ttaaacccca ggaacatacc aaggtcaata gttttccttc cagctcactg actcttaaga 840
aaacgacctt tatgcagggg actaaattct gtaaagacta ttgaagccat agttctaaaa 900
aaaagttaga aacgtccacg tgtgtggcaa gtagaaagtt tttgtttgtt ttaatgtgta 960
aggaatagct caggtccagt tnccaatgta agggaaacaa gcagaaggtg tttcattcct 1020
tgataagcta acgacatctg acctaatgta tggaaagtgc gtctgtgcgc atgcgtgtgt 1080
gtgtgcgtgc gtgtgtgtgc atatggcgag agtatggcaa tcagaattca ggggatgtga 1140
tgctcctttg gtttgtgtgt tcagtatctc tatggaaaga gcaggttgat tgctaagttt 1200
actttgttat ttgagctttc agagtgagca tttaaagatc tattccatac acactgttga 1260
ttgtctgggt cccacccccat ccccatcccc atcccccacc atttcgttgg ttgaaattta 1320
agtttaaatg tcacctgagg ccaggttctg tggttcacgc ctgtaatgcc agtactttgg 1380
gaagctgatg caggaggatt acctgaggcc aggaattcaa gaccaccctg ggcaacacag 1440
tgagatccta tctctattaa aaatttaaaa attagctagg catggtggca tgcacctgtt 1500
gtcccagtta ctcaggaggc tgaggcagaa agatcttgag ccagggaggc tgaggctaca 1560
gtgagaataa aaacaataac aaaaacaaaa aataaaaaat aaggccaggc acagtaagta 1620
gctcacgcct gtaatcctag tactttggga ggccgaggcg ggtggatcac ctgaggtcag 1680
gagtccaaga ccagcctggc caacatggtg aaaccccgtc tctgcttaaa atacaaaaat 1740
tagccaggtg tggtggtgcg tgcctgtaat cccagctact tgggaggctg aggcaggaga 1800
atcacttgag ccctggaggc ggaggttgca gtgagccgag attgtgccac tgcactccag 1860
cctgggtgac aagagtgaga ctccatctca aaaaacaaaa caaaataaaa taaaataaaa 1920
taaaaataaa tgttacctga atattcccac ttaggtatga aattgatgtg cttgctttgt 1980
tttatttcca tttgttcttt ctgttgttat tgttgttttt cagtgaggaa tcattaaaaa 2040
tatcaaatta ttagctgtgg agactctcat ttacctaaga ataatctaat aactaatttc 2100
ttttctaatt tttaaaccaa agttcagtgt gagatttgtg tattaaaaag tgcaatttgt 2160
atcacaatca gtactaagcc ataaatcttt atcattgtta ttgatttaaa attatctttg 2220
agccttgata tatttgcaat tgaatgaaaa taatttgtta aggngcttat ttnaggatcc 2280
atggcagtca gcacggcaaa acacatgcta ggaaagtaaa tggttagttt taaattttaa 2340
gacattgcta cggacataaa atttattagc ttttttaacc agttaaccaa ttttttacct 2400
tttttaccaa ttgccaattt ggggctgaaa atataaatat atgtaatttg tattatattt 2460
atattatata taatttgtat tatatttata ttatatacat aattcaaaaa tggaggtatc 2520
atttgtatat acaatgacat atcttattga tgaatgtaaa catgcattct caagacagaa 2580
aattattaaa attaaatgac cagattttat tacatgtttt gcatcatgat atatgtgctt 2640
tattaatttg atttttgcat atttcagtat tattctacat tttttgccag gctttactct 2700
gagcataaaa ctgggtgctg ccatttaatt ccaaatatat aatgatcaac tgtctgctcc 2760
aaagctgcac cttccaatgt taccaccaat tttattatta aggattgtta attccattga 2820
ttnatagttt tcaataataa tgaataatat tattcattaa tcaataatca actgataatc 2880
aataattaat taattaatca attaaacaat aatgttatga ttattcataa tccattattg 2940
tatactaaaa acatatttct gatggtatgt ttagctcagg ataaagaaga catgggctaa 3000
gataggccct ctgtttctgc caaagtagca gagaaaagtc ttctttccta gagttttgtg 3060
ccctaagcac atttgcaggg atgggttcaa agacttgcag agtgtgtact tatattctta 3120
actctataag taggaggatg ctcatttttc tctaagatac acacaacaca cttagagaac 3180
agaaaatgca ctgtattata ctaacttcac aggggttaga ccgcagcaag tcaatggaac 3240
acagggagca cccaacgaga arctgtcctt gaaaatgttt tagggaggaa ttctaaagtc 3300
ttgcctttca acttaactgt gtatcttcat ttgaattatg gaaccattgt tcatgagtga 3360
aatctatttt tatgttctga atcttcccat ttaaagacat atgttttctc agcttttaga 3420
caataacatg atctaaaatg tcaaaataat acattctgct gaatctcagt atttactgag 3480
gaaatacaga aacatggcaa aagttaggaa gaaaaatgtt tccttttttct gctgtccaca 3540
aaagttggtg gaacatttat gactgcaaaa aaaaatgagt tattaacact gttttgattg 3600
aattcaacag atgctctgac tttcttatat atatgtgtgt gtatgtatac atatatattt 3660
aacaactata aatatttata tgtaacaaca ctttcacaag atgccaataa atttagtatg 3720
agcatttaca tatctaaatc tttctttggc tctagaaact gatgctatgc caaccagaac 3780
aaagaaatag tagctttcac tactgtcact gctaataaaa ttcagcatca ttacagctta 3840
tacaaaattg tacttattag cccaatttct attgcttgcc ttaaaaaaat gtatcggaga 3900
aaatggatgc cattagttta gtttgtagat taaactgata ataataatgg caaaaccttg 3960

atcaagtaaa taaatcccac taaatagaac aggaatgtgt tgctaagacc aaggccattt 4020
ggattcaccc tgagcttgtg tttagaggca ttctttcatt cattcattca ttcattcagg 4080
cactaatggc tgagtcatgc cagaggctag gcccctcctg cggagagttc actgctgcct 4140
aaagacagac caggttcttg cccttatgtt aatattcggg tcttgcctag tcagttatat 4200
aaagttcatt aaaatttgct tacataattc aagcaagtgc tcagttttaa atgtctgtgc 4260
cacacaattt gacaatttac ataatttatt tcagtgctaa agaagttgac aatcgctgtt 4320
taacttcagt cgggcttctc ctaagcgggg cgaacacaca caggacatgc acaagataat 4380
ctgttaaagt atgacaagaa aataataaat tctacttgca gttataattt tatcctaacc 4440
tttgcaatca cttgtgctct gtgtgtgttg tataatgtac acattatata acagttcatg 4500
tgtatataaa tgaatattta tgtaagggaa atatgctaaa aatcttaaat gggtggaata 4560
actactaaaa atgtttagca agtacaatta aaacatatac aagttagtgt cacttctgta 4620
taatttaata gttaaatagt tgtttctatg gggaatagta agccacagag agaaagaagg 4680
tcttaagacc gggaccagaa aaataagctt cttaattgga ggcggcggtt acttctagtg 4740
ataggcgatt gtttttttcca gatataattc tggctccttc ctaattaaga ttagtgttac 4800
tcatgtcacc aatttgcagg gtttcaagct tgtgttaata agatcacaaa cattgtgagc 4860
ctttgccatc tttaaaatct ttcactctaa agcaaaacgc acataacagt tgccgaagtg 4920
ccttctttga gcttctttga aaacagccgc attttctttg agctatggag agcagcatag 4980
aacatgtttg aatccccaaa gcttaacccc agaaaagata tttcttgcaa gccacaaaca 5040
attctacact tacagtatca tgagttaata tttacctctg cataactggt atagaataaa 5100
acacagtttg atgtggggtg gcggggtgta gggtaaaatg acctaaaagc ccaccctgtc 5160
tctgttacat tttgctgtgg gactttgtcc atattgctta cattctctga gtctcggttt 5220
tcatattcat aaattagaat aatatcactc acatcacaga taccgtgcat tgaaaacacc 5280
tggcaaaata actgatagta aatagtttctt ttttatttttt ttacttttta ttttttgaga 5340
cagagtctca ctctgtcacc caggctggag tgcaatggtg cagtcttggc tccctgcagt 5400
ttctgactcc tgagttcaag tgattctcct gcctcagcct cccaagtagc tggaattaca 5460
ggcatgcacc gccacgccca gctaattttt gtaatttttt agtagagaca gagttttgcc 5520
aggttggcca ggctggtctt gaactcctga gctcaggtga tccacccacc tcggcctccc 5580
aaagtactag gcttacaggc atgagccacc atgcctggcc ttgaattttt taaatttcaa 5640
tagctttagt ggtgcaagtg gtttttggtc acatggatga gttgtataat ggtgaagtct 5700
gtgattttag tgcaccggtc acctgagtag tgtacattgt accctacagg tagttttcta 5760
tctctcaccc ccttcacaaa ctcccccatt ctgagtctcc actgtctgtt gtatcaccct 5820
gtgtaccttt gcatacccca taggttagct cccacttata aatgagaata tgcagtattt 5880
ggtttttcat tcctgagtta cttcaatgca aacttgctgc aaaagaaatt ttgttctttt 5940
ttttatggct gactagtatt ctatggtgtt tatattatat acatttcatt atctccttcc 6000
ttcccttgct gtcttcctcc catgctctgc ccttcctccc tctctttctc atatcagaag 6060
cacactaacc tccaccccac tcctctctct gacatgccca tctcactccc tcacatgccg 6120
tcctcttctc ttctccagaa accctcagcc cccattgact tctgctccct ccacacggag 6180
gtgcactgac gggagcattc acagtgggat tcatcttacc ctggctcctc raattttaca 6240
gcactatttc tgatgccagg gaaaatgtct tatgatgaaa tttttaacct gccctacacc 6300
tctgctcccc aaggcaccta tctactgtca gactccaaag ttggctctca gtgaaaaatg 6360
tgggattaac agacagattg gatggtacct aggcagccag tcctctgttt catggtaaca 6420
ggctacaagt ctgtatttca attagaatac tgaagtgttc actctgactt tttaaatatg 6480
taaattctaa tagaatcact ggcatttttc tgacagtaat gcagaccagg tttaaatagg 6540
caacatgttt aaagaaccac gtgacacaat tctactccat tcccagggtg ccggttggct 6600
cttaatttac aaaaggggtt tgcattcata cctttcccag cttctcacta gcaggacaca 6660
ttaagataat gcagaaaaca acaaagatag tgtggtgtta gctgctgttt cttgaggagc 6720
aaatgcaatg acaaaatcag aaatgctggc atctgtggga aaaacaaaga atgcaaagag 6780
cctgctccac tgaggaacag cagattttct ttgagcaaaa gcagattatt cttgtttcaa 6840
ttataatttt tgtgactgtg acattggtaa agtagggtgg caatcatgca ctcttggtac 6900
acaagtgacc tgacaatatg gccaagaagt aaaactttta gatacatacc aaaagcatta 6960
tatattctag ttctataatg tgcacagcta tgtaaaagta tcagattctt agataactaa 7020
ctatagttta ttatgtcaca ttttccatcc tttactttgg attatatgac aaagttatgc 7080
attaactttc ttcagactct ttttttgcc catttctact aagtgaggct gttacagtaa 7140
gttccttct ctttggtttt atgaagaaac gaatacatct gcattttata gtgaatttac 7200
tgattactta ttatagctct actcagtgcg ttggtattat tggtattttc taaatagatt 7260
gtagattatg gaagataaca ttcatttatt aatcatcaag tgctccatga aatcttatat 7320
gagttctgga aaagaaggaa agcctaacac attctctctt ctcctatcct tggtgaatat 7380
attatccctt tatatcctta gattagtttc agatttctta tttaagactc aattccattt 7440

ccctttcttt agaagactga tttcccactt tttaaaccct tttcaacatt ctcaactcac 7500
tcaagatgtg gagcccaaaa ttgaatttat attgaagtgt tcacttgctg ccttttttaga 7560
gatataaatt ttaataggat cactggcact tttgtgacag tccatacagg ccaggttaaa 7620
taagtggtat gtttagagga catgtaatac tctgcacttc taaggcattg cttgttggct 7680
gagagtccac aaaaggtgct ttcatttact acgggcccat tccgactcta gataaggcta 7740
ttgagttata tccatccacg gccaacactc agaagtagtc ttatggagtg actttcttct 7800
tttttgatgc ccacagcaga gctcccacca tcttcgtcac taacatgata atccggtgaa 7860
ggcagcttgt taaaagagat cttccttcac accaaaggaa acgcttcctt atttactgtg 7920
aagttaattc actggttatt atcatcgtta atattcattt ctggatatat aatagaactg 7980
ttctggaaag gtatgaatta gtataacctc tctgctcaac acttttgcc acaatcccag 8040
ccaaagtagt gtgtccgttt aaataacagc tataaaatat actttgccct ctgaagctct 8100
gtggccttcc atgagctcag aacaataaac cacaccattc cccatctttg tgtgacaatc 8160
tttctcagct tgcaacccaa tcccatattg tgctttagga cctgaaccat ggggtctttt 8220
tggaaggaga ggttcacttc atgaagtgga cttttaaaaa tttatttctt tagtttttgt 8280
ttgtttgttt gttttgtttg tttttgtttt cggccttcaa taacggccac tgggttggtc 8340
atatgaaaag ggattcttag gatttaatat gttgggggct catcagggtt cctggtttga 8400
gtctctgctc tgggcaggat ctcagggcca ggtggactgg ctctcacgct aaccaatcgc 8460
ggggcatcat tatgcaagcc caaaggccat gttactagtt tccagtgggc attccactga 8520
cggtaaattt ctgccagata catccagggc actggggata caagaaggca caaagcttgg 8580
ccttcattcc aagagcatag ggtctgggaa ggaggcagac gagaagacag catcacatgt 8640
actgaactgc cgaagaagag ctcattgcag ggtctagagg gaatgcagga aaggcttcca 8700
agtgaggtca cacaggatgg acaggaatta ataggctgag ggattcgtga gggaggtgga 8760
aggaagagcc tggtgcagag ccaccgaggg cacgctgcac atcgagtgac ctgcttgtca 8820
ctcctgtggc cagagagcag agtgccgggt gggagtgggc agagatgagt ctcgactgct 8880
cagcagggca aggtcgcaga gctgtgaatc ggttaggagc tttgaacatt ctcctgggtg 8940
ttgctgtggg atggggtggg gtgctgaatt attaaaaatg aagtagtgga ataatctgga 9000
ataatcaaat taattttcta tagattgctc taactgcagc atgaagcagg agttcacaac 9060
tgaaggcaca agggtaggct ccacggggta tatccaaggc agaaatccaa gtgagagatg 9120
ctgatggcgc gagcagcact ggtgtcagta gaaatcaaga gatttgggca gacatagagc 9180
tattgaggaa gcaggctcac agggcgtggt gattgaagag ctgtggagcg tggaagaggc 9240
acccggatga cccccaggtt tctcacctgc ttccctccga aaagaagagg ccgaattcca 9300
ctttagagtt tgtagtgctt gaggtattga aacagagtga gagagggaga gaaagagaga 9360
gacagagaaa gagagagaga gatcagcatt ggtaatgaag atttaggctt cactatttta 9420
aagactacaa ttgaatcacg aggatggacg gttgcccaga aagaatgtgt agaaacaagc 9480
ttggaacaga agccggaggg atactaacat tttggggaat ggcagggaaa acaaacaaac 9540
aacagcaaca gcaaacaaat gaagatggag aaggaggggc agaggactaa gagggacacc 9600
aggataaaac aagtcccagt ggcatttccg gaagctgttc aatcaaccat gatcagggct 9660
ggcaagaggt caaataagac aacaactgat tttccagctg gatttgtcag cagaggggcc 9720
aaggagcttg gaaagaacaa tctcagtgga gtggttcgag ctgaggccaa atcatagtga 9780
gatgaagtga aagataaaac aaggaagata ttgactgtta catgagacgt ttattaatga 9840
ggaagagaga aaaagagaaa actaagttgc ytctgtgtca tagttaggac acgttttcct 9900
ttgcataacg ctggagacat attgacaaat gcttcttagg tttccctttt ttcctaagcc 9960
ctgtgcagat tatctctgga tgggcacatt ctctatttgc gaaagcacag ccgagttgat 10020
ctgcttttca ccttctgtac aatcatatgt ctgggcagct ccgtggtgcc ataccctgat 10080
tggccaactg ggcttgcgtt ggccctgtga tgttcagact gattccctct cctgtataaa 10140
tggagtctgg gatgctggcg tggatgggca ctgcaggagc ctcattttgg tgttgagaat 10200
ggtttgggtg gactgggaaa tgtgggacag agccaacaag ctcaggaggc cctgaaatgc 10260
aagggaatag accaagtgtg atgacaggat tcaaaaagtg ggtcaccacc agaaaacagg 10320
aagacatttg cgttttactt caggaaatgg agccaagaca aagccctaga aggcaagggg 10380
tgctgatgtc ataagacccc ccacaaggga tcaagaagct cagagcgctg cttaccgccc 10440
atccttaagc ttacttcaca gactcagctc agcctcaagc agtggggcct ttcttgtttc 10500
cctttgagaa tatatcacga tttccaattt ctaggtgcaa tgtgctttca ccagacactg 10560
acacagacat agcagaaagc agacattcag acataggaac gtgaaaattt attttgagtt 10620
tcaccctcac ttaaaactgt agcaacatgc gttatgcgtc aaagtgcatt agcctgaggc 10680
ggttgctgtc gcagactaat gcttacataa ccaattattt cacccacaca tacccaaaac 10740
tcaggccgct agcggggtta gagctggcag aaacggatct aataaaatgt atcaacaaat 10800
gctacaaatg tgaaaggaaa gttagtcctt actaataagt gggggaaaag ggagagcagc 10860
tgcttagcct cttgatttga agctgacaac cattttaat atctgacatt tttctttgtg 10920

ataaaatata tagccaacat gatatttttt cagcaggcta acatatattt acattagcaa 10980
tcttctacct tgctctaaaa tagagagatg gattttggag atgggggtaa tatatattta 11040
aaaagtaatg agaagctgac ctgctggaaa aatattaatc atagggcatt ttttgaaagg 11100
ttctgcacag attagctatc ttcaaatgga atgcccagaa ccaagagagg acatgaggac 11160
accacacaag cacacctgcc agccgtctat atggcaccat tgttaaccat ggtgatcctg 11220
gtcccgngta gnatttctat tcccaaatgc atgggctact tcaggattgt ccagatttgc 11280
atgtaacgca tttctttcta gagttcgtgg cttcacatca ctccccgtaa tcaggaagca 11340
aagtactccc cctcggtctg tctccggagg ctgtgccgtt ataaccaaag ctttaaaaaa 11400
aaaaaatctt cattaagagt gtgaaaatga gtttgctaga tgagctctct tgggttctcc 11460
ttggtctctt cagcctttgc tctccctgat cacctcttca aacaggcctt tgtgaccaag 11520
ggattctcag ctgagaatcc aaacacaggg tagatgtgga cgtaggtctg gaggtagagg 11580
gtgggggctc atacagccca ctctgcagaa ctgcaagtga gtttcaaaat gaagtgactt 11640
gcaaaaaaga aaaaaagaaa aaggatatgt tcggaatgaa taatactcaa gtgatacctt 11700
ccgaataaca tggagtgtaa tttcaacagc cgcccagggg ccctaccttg ctcagctgtc 11760
atctgcatct ttctagaccc cacttccgac gttaacagag gctcagctag gtggtctcta 11820
aggctttcca ccctggaatg tctcacctta gtgactccag agaccccgac gtatccaatg 11880
ctcccttcac tttctgtcct ctcagaagag ttcctgttac aagagttccc actgaaaaaa 11940
actatggact gggctgtgga gagagttgaa ttccacttat ttgatgccta atttccctgt 12000
atacgtttcc ttatttgtaa aacatttccc aaacaagtct caagggcttt atgaggaaag 12060
atagcaagag agaaaatgct tcaggggaaa aagagaaaaa tcgattcaag tattaagtaa 12120
aaatgatgct gtcatttgga ccatttttct agtgtagtct gctcctcttg cagacagcac 12180
cttgagaaca ctgtatggtg ggcagctgtc cagcaaagat tgtgacagtc aataagtcat 12240
ttccagagga cacagtggag gagcgtgggg gcggtgggcc atttgaaata ccctttcaga 12300
gcataatttc ctgacaaatc aagctgcttc ttgggtagat ggaggcactg gccatcaagg 12360
ggaagagtgg gtggatgtcg gcgagccatt actctgtcac cagagacctc gcacacattt 12420
ttattccttc ccacagttat tctttcgttt catataatta tttatactct gcagtgacac 12480
atagaaaagc aatttaccta atatttctct ctataggaga aggccaagcc attataaaaa 12540
agatttctag acttctttgt actccatagt tcttatgaaa taagacaaat atactcattt 12600
ttcatgatgt gcttttgttt gaagttcttt attactttta agatttagtc aatttgttct 12660
tctagcccgg tgccaccaca aaacatcctt ttcaacccct tcctgcaaaa acttctagaa 12720
agacgttggg aagtgtcttg gagccatggc cttctctcac cttcctaaca taggaatctt 12780
cctcatcgtg ttttgacaag aggtattgaa agtctattgg aatttttcta gctctagaga 12840
actcggcaca tttgaagata gctcattgta tttctatgca tctcttctgg caggaaagct 12900
cgtctttata tcacgctggt agctacctgt ttgtttttc tcttgtcttt gttttgtgat 12960
tccacaattt attgtttaaa tccatcgtca ttggcacctg gccgtttctc agacacgaga 13020
taactgtaag aacctcaccc ctcgtttgct cttagccgca gtatattctc aggtattctc 13080
cgttcttcac ataacacagt tttcaggtgt ttactaacgt gctatttcac ttttcaagta 13140
atcattttca agattctaga agaatttttg tttacttccc atgcgaactt ttaccagttt 13200
attctgaaat atttttagca aatgtgctgt atgctttgcc tcttttattg taaacacatc 13260
tacacagaga agataaagcc tttagttatg taacatctgc ttctcatcct taatctctta 13320
agtagcaata aaatatttct cctccgtcct tcggatttcg attcagctca catggtttcc 13380
cccacttgtt ttctgatgta tcttaccccc agagctaaaa ttttagaaaa tatttaatac 13440
tcaaatgagg aatattcatt gcacactcaa agcccaggag gtagctcata acggatgcca 13500
ccgtggagcc tggccggaga ggtcgtcata gctcagtgta taaggtctgg gattctgccg 13560
gcagctttgc aaatgatgct cgatcacttt tcttcataac taactactac ctgatactta 13620
aaaaaaaatg ctgtgatctc ttactagttt ctttttcttt tcnttttttt ttttttttg 13680
nagttaaaaa aaaatctgca aaggaaatat agcggaaata gaatttaagg agccagaata 13740
aaaatggata tgttcccatc gggcaatgct gaggaaagtg gttgcaaaga ggatggctag 13800
atctgaagag actccagtac tggacgcccc accgtctgcg anngagagga gacgttgttt 13860
cttaagactt tatggctgca ggatgcgatt ccctattcag aacccatttt aactggaata 13920
acggtggaaa ggcaacgtgt gagggagcgg tgggaatggg gaccccaatt tggccaatga 13980
aaacatgagc cactttctgg cattacatag ggcactcctt aaagaaaaac aggcaactct 14040
agactttaga atcccagaaa tgtgcggaaa gcaagctgtc ctcataatgg aatgttattt 14100
tttgaactgc aggtataagc ctatcctgct tcctctagta cctgagaaag gttattaagc 14160
ccaggaatca gaggatacat ggctcattcc tatactacag cttagtttac ataataaatg 14220
tcatgtcata ttacgtatca tgtcatatta cacaaacgtc aatgtctatg gcattttgac 14280
aaacgttttc aacttcccca tggtttggtt aagaaatcat ttcacttttt cttctgaagc 14340
tggtgcttcc agcctcttgc tgccggcacc acctccacct tcacctgtcc ccctgaggca 14400

gcctcttgct gtcctcctgg ggcacacagc cacagcccac ctccgtttcc cagttggcat 14460
aagaattctt agaggtttct tcggctattg taacgttttc ttctagtgca gtttttcagt 14520
gtacactgtt acgagaagac tcattcaaaa gacctataag aattctaatt atttgtaggt 14580
tttactaaca agttacatgg tgattgtgag ccattgatga ctggcaaaga aaaattactt 14640
ttggccattt aaaagtgtat ctcactttga tatttatctc attttacctc taccaagtca 14700
ccttgatcac agaataaagc gtcattttga tcaacctaat gttatgaata aaaaaataca 14760
atcctccttc taccaaatag atattgaccc ggggcatgga aggccatgct gattttaggt 14820
tcatctgcaa actcccttgt gatttcataa gtgctttaaa agtagttttc agattaaata 14880
taggataact attaggaaca cagtctttgg agccctacag aacatgggtt tgaagtctgg 14940
attttccatt tccattacct aatagtayta ttacttaata ttattcctgt tcaaaatgtg 15000
agtaatagtt atggtcaaaa gtgcatgctg agaatcacat ggaaaaaaaa gtttacagct 15060
tacttagaaa agagtataaa gttgataaat accagctatt attcttgtta ttattaggta 15120
tttataatct cttaggctac ctttaactgc tgcgcctcca tttttctagg taaaatataa 15180
ccggcaaaat gttacttgga taatattaac cctaaaaata gataagtaaa agccattagt 15240
gccaaggacc tggagaataa ctgaatttca gtaacctgta ctgcaaattg gtacatctgc 15300
cattgttgta tttgaattta agatcagctt attccttcgt gtcagaaaaa ggcaattttt 15360
tcaatgtttg ttttcccaaa tagccaccaa aacaaagaga tgaatgaagt cccagtcctt 15420
tcacatttga tgaaattaca taaatacgta gcaaacattg atgtggcttg cacatcatcc 15480
agaaggttga agctgtggct ctgatgaggc ttccctccta ctcccaacca caccacagca 15540
tatgatgtct gctctatgtc gggtgtttct gggctttcag acagtgagat ttttaatgca 15600
tttggtgtga gtcatgaatg taaatgtcca tatctgcctg ttctgtgcct ctcaaagtcc 15660
aagatctaaa cagcagtttc ccaacccctg ctgggccatc tttataaagt gcttcgcgcc 15720
atctagcgtc ctatggaggc atagacgtgg gactccgtgt ggagggaact ggctcatcag 15780
ccacgttgca agtaactaca gcacagaaga gcaatagagt caattattta ttttacttta 15840
gatatcgctg aattttgaaa aattaacttc ctgcttaaat ccactgattt tcaaataagc 15900
cacataaaat taaaggtcaa aataccttttt acattctatt agggatgcaa tcaaatactg 15960
ttttgctttt attgcggaga ctttcgttgc tgtgttttta tcacttgcag ctgtcgttgt 16020
gtaaatacgc tttctcacaa tgagggctct cttaggatcc acttgaaacc acagcacgct 16080
tgcacgcttc tcacagtgcc tctatcactg taactgttgt cacgcctcta tatttttcat 16140
tcttctcttt ttttcagatt gtctacaaag cctggctctg ttcccagtat tttgaagtca 16200
cacagtttaa ctgcagaaag acaattcctt gcaagcaata ctgtttggag gttcagacga 16260
ggtgtccatt tatattgccc gacaatgatg aagtcatcta cggaggcctc tccagtttca 16320
tctgtacagg tacagtgccg ggtgggagtc tgtacaccag tctccggtgg ttttgctttc 16380
ttgtgtgatg tttgtttgct ttgctgtttc ctttcactga tataaccttg aagatgcggc 16440
tggtagtttt ccgcactttc actaatagaa gcaccgaaag ctcccctcaa caggtctgga 16500
aatgattcag cttctgtacc acatggtcta tctgtaactg agaccacagt tattcactgt 16560
gtgaaagaag aaatctgatg gcaaaatatt agcaatcatt agatatactt acatgtgacc 16620
tagtataggt tagattcagc ctgcattgcc tttgaattcc ataagaacag gagatgtgct 16680
aaggccagtg aaataatgct tttcaaatta gtcagaagtt tatgttctct tgcctatttt 16740
cttttatttt attttctgag aatttttatg ttactttatc tgtaaaaagt attaagagca 16800
ttaaaaatat ctgcctaaat tgtacgtgtg tgtgtgtgtg tgtgtgtcnn ntattagagc 16860
cacacaacaa gtctatccat taaacgatgt ttacttcttt cagcaaatga gtcagactgg 16920
gcaaaacacc aatatcagca ctccttttct ggatatttat aagcattaca taatttagac 16980
agaataagat ataaagagca agagcctttt tttaaaaaat anaaatgata attaaatggt 17040
gagaacaaga tgctttgcca gggtggtgtg ataatccgag tggtggctct ngcattctct 17100
tctataacaa taatgctata aggcgtccct ggaattacgt ggctcaagct gtagcacgtt 17160
ttgttttcaa gtgttttgat aaaacaccat catatgtgta gagacacatg aaaatgctct 17220
tctgacatta gacttgccaa actcctctaa aacagagtag catattaaga tgctcaacat 17280
gagaatttat caaattattt cagcatcgct tatttacata cgtattcatt agccacagtg 17340
ttctaagtga taagctatca agagatagtc tgccaaagct cgccctaaga actggatgag 17400
tatttctttc ttttttttt tttgagatgg agtctcgctc tgtgtcaccc aggctggtgt 17460
gatctcggct cactttaagc tccgcctccg gggttcaagt gattctcatg cctcagcctc 17520
ccgagtagct gagattacag gcgtgcacca ccacacctgg ctaatttttg tatttttagt 17580
agagacggtg tttcaccgtg ttggccaggc tggtctccaa ctcctgacct caagtgatcc 17640
accctccttg gcctcccaaa agtgttggaa ttacaggcgt gagccactgt gcccagcctg 17700
gattagtatt tcttatgctg cccaagcttg tggaaagaac acgtgactga aggtcaggag 17760
cattggcctt catcctgttt ctattgtaca ttctctcaga ggcaccaccc cttcactagt 17820
aaattagaaa gtgcaatggc caaaccctcc cccatgtgga tatgctgcaa ggattacaga 17880

taagagagaa gggcaagtta tgtcattgac cagccatagc cgttgcacac gagaaagtga 17940
aatgcagaat gatttcacag gcctgtgtgt tattctactg acttgatgct caagtcattt 18000
tttatgtagc tcctctctgc tggaggggga ggaggggaag gaaggaggga agagggaaag 18060
aaggaataag ggaaggaggg aaggaggata tcaatatctt cttgctttga gtttgagaca 18120
aaattcncca gacacaggct attaattcat attgaatttt gcatacaaca ttccacaaat 18180
aaccatgaag ataaggcctt catttttttt ttcttgtggg acaatgaggt gtctgtgaca 18240
tgaggacttc agagaagcta ttcgattttt atgtacaggt tgtgtttatg catttacact 18300
cacattggct tttgtcctag agaagaacaa tagtttttga accaagttct caaagtagac 18360
aaaaaaccca aatgaagggc gaggtgtttg cgtttatctt ctttttccta catgtatctg 18420
tatttgtgaa tctgaaatat atgtttgaat gttcacccac ttcctccata cacattcaga 18480
atgccagggt agaattaaat ctctcacttc acaacatggg cagagaatcc agtctgcagt 18540
tttaattgtt ttcgagtttg gtaaaaacag cttcttcata gacatagcta cgtcattaag 18600
gaaaagtggc aggaaaagag agatttatca gatccagaga aaagtgccat ctccgtgaga 18660
ggccccctag gataatctca tcactgaaca tttggaaacc taagaacagt agttcttatg 18720
tcactttcag ttgggttaat gttcatttta tgtttaaatt gctcgaaaat atatggaata 18780
aattctgagg ttatttcacc ctgaagttct gtaaaacaat ctgacagaaa aagataataa 18840
ttttcatatt gatcttcttt tctaaggtgt gacctatgcc tctttgaaga attctcattc 18900
atgttgataa ctagcagcca tcatttccca tcatcggtta caggtgtccc ttaagagtgc 18960
actgctgagg ccagatgcag tggctcatgc ctgtaatcca cacaattttg gtaggctgag 19020
ataggagaat tgcttgaagc caggggtttg aggacagtct ggacaacgta gcaagaccct 19080
gcctctacaa aaaattaaaa ataaaagaac tagccagaca cagttatgtg cacctgtagt 19140
cgcagctatt tggaaggcag agacaggatt gcttgagctc aggtgctgga gattgcagtg 19200
agctgtgatc ctgccactgc actcctgcct gggcagcata gcgagaccct gtctcaaatg 19260
aaaaagaaaa tgaaagagtg cactgctgga cctgagcaag gagatttcta ctcctgtcca 19320
tcacagctgc ctgcccgttg cttataagag tcccagacat gggccccaga atgggtttca 19380
tcttggatga tgttagaata gaggacagct cccagaggac cactggctaa actgtggagt 19440
ggcttgtcat gcgtctaagg aaactagtaa gacatatgtg catataattt gttcccagat 19500
tttaagttgc acatttttgg atgtccgtct cctacaaatg tacacggatt tttaaatagt 19560
ttacattata aataagtttg caagtaaatg tgagccattt acattctgtt ttttttctct 19620
gaaaacagaa taataaaaag accagtgtag ttatagcatc atttaatctc atacaaaata 19680
ttttaataaa tatatcaaag tttaagggaa aaaagaaatg ggaagggaga tggtatgccc 19740
agaataaaat aaaaaaatga gagtaggtta tgaaaccaag taaaatgcag taacttcatc 19800
aaaaagaatt caccaagtaa ggtgaccttc ctcttgcctc cagcaatttt tctttttgaa 19860
aaaaatcatc aagcatttga tttccactct agatgttaaa atgcaatcat ttctcactaa 19920
gaattaaagg aataggtgga gtttccttca acttcaacag atttaattat aatggttttc 19980
ctactatttg aactgcatcc aattcacagc ttccagaagg acggagaatt ccctctagga 20040
tatcgaggat tcttcactta cttttcttat tgacctcaaa aaaaagtatt ctgtaagcac 20100
gtaactgcat atggcctgat gacagatact gtccatgtga gcatcagttt tcttcaaggt 20160
gcttctcctt agtgacaaac cagtggcatg gtgattcctt ttcttagcgt tctctgtacc 20220
cagaatctta gagatctcaa gttcttcctg tcattgtcyt attggctata tactgatacc 20280
taggattcct attattcaca aaaaagggaa tatcaccccc tggaatcaat gaacaatttc 20340
tgtaaatgat caggagttat ttaccatttt ggtcacactt actaaattca gtatctcgtg 20400
catcatttct ttatggtgct cacatcacca tgtaccaaat ttgaaagttt taaatgtata 20460
tatttttgat catctgctac ctatgatcct ttagtaagcc aggaacttac tttaaaaaat 20520
gaaatatctg agaatgcatg tccattacta tagaatgctt ttgattgagg atgttacaga 20580
aggtcatgac caaatgttct aaccacggat cttgatgaca agcgcatccc cgtgcatatg 20640
tttaattcca attctgtctt aggagataaa aggaaagaca ctttgcctga gatttctctt 20700
gaatttttt ctattaaaga ataaaactga cacgtgacta aagaaatgtt ttaaaaatta 20760
attggaaaga aattctgagg tgctgtcagg gtgaaacatg tcatttaatg ttaggcatta 20820
ttgagctaaa atttgtcaag gtgggttctg ttgggtttgc aagctcagtt cgcataatgc 20880
agtgctattt tagaaactca gttgcttcat ctttaaagtg aggggtggn aagtcgtttt 20940
tggattctac gatgtcaacc cngtcatcgt ggtaattacg tgggcttccc tctnccacac 21000
tccctcgcct cattccagag tcccctggag aaatccttga ttgcttacct ttaacagtga 21060
accaagctga agaaaacaga ggcagcagag gagcacaggc tgtgggtgct atggtaacaa 21120
acattaagaa aattatcatt tgattgatag ataaaataga ccagccatga tttactgctc 21180
tcttacagag ggacaattat tgaaggnaat aaaagtaaaa gttggtctgc tgggggttac 21240
tgacaatgga gataaaacat attttaagaa ttctatgt 21278

<210> 3
<211> 21636
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> 5537..9359
<223> exon 3

<220>
<221> misc_feature
<222> 16330..18329
<223> 3' regulatory region

<220>
<221> allele
<222> 8277
<223> 99-13821-332 : polymorphic base C or T

<220>
<221> allele
<222> 15915
<223> 99-15215-60 : polymorphic base A or G

<220>
<221> allele
<222> 16053
<223> 99-13525-395 : polymorphic base A or G

<220>
<221> allele
<222> 17032
<223> 99-13526-368 : polymorphic base A or G

<220>
<221> allele
<222> 19401
<223> 99-15208-87 : polymorphic base A or G

<220>
<221> primer_bind
<222> 7946..7965
<223> 99-13821.pu

<220>
<221> primer_bind
<222> 8454..8472
<223> 99-13821.rp complement

<220>
<221> primer_bind
<222> 15475..15495
<223> 99-15215.rp

<220>
<221> primer_bind
<222> 15943..15960

<223> 99-13525.rp

<220>
<221> primer_bind
<222> 15954..15974
<223> 99-15215.pu complement

<220>
<221> primer_bind
<222> 16430..16447
<223> 99-13525.pu complement

<220>
<221> primer_bind
<222> 16950..16970
<223> 99-13526.rp

<220>
<221> primer_bind
<222> 17381..17401
<223> 99-13526.pu complement

<220>
<221> primer_bind
<222> 19315..19333
<223> 99-15208.pu

<220>
<221> primer_bind
<222> 19797..19817
<223> 99-15208.rp complement

<220>
<221> misc_binding
<222> 8254..8300
<223> 99-13821-332.probe

<220>
<221> misc_binding
<222> 15892..15938
<223> 99-15215-60.probe

<220>
<221> misc_binding
<222> 16030..16076
<223> 99-13525-395.probe

<220>
<221> misc_binding
<222> 17009..17055
<223> 99-13526-368.probe

<220>
<221> misc_binding
<222> 19378..19424
<223> 99-15208-87.probe

<220>

<221> primer_bind
<222> 8258..8276
<223> 99-13821-332.mis

<220>
<221> primer_bind
<222> 8278..8296
<223> 99-13821-332.mis complement

<220>
<221> primer_bind
<222> 15896..15914
<223> 99-15215-60.mis

<220>
<221> primer_bind
<222> 15916..15934
<223> 99-15215-60.mis complement

<220>
<221> primer_bind
<222> 16034..16052
<223> 99-13525-395.mis

<220>
<221> primer_bind
<222> 16054..16072
<223> 99-13525-395.mis complement

<220>
<221> primer_bind
<222> 17013..17031
<223> 99-13526-368.mis

<220>
<221> primer_bind
<222> 17033..17051
<223> 99-13526-368.mis complement

<220>
<221> primer_bind
<222> 19382..19400
<223> 99-15208-87.mis

<220>
<221> primer_bind
<222> 19402..19420
<223> 99-15208-87.mis complement

<220>
<221> misc_feature
<222> 110,4287,4291,4453..4454,4506,4520..4521,4558,4580,5958,17188
17327..17328,17415,17917,17944,17962,17976,18224,19785,20084
20138,21414,21428,21433,21463,21480
<223> n=a, g, c or t

<400> 3
aaaaaaaact ctgtgaggtt ggtactgtaa tgtcaaacag caggtaatga ttcactagag 60

atttcaaata gaacagctta taagcaaaat atatcagaac aacatttcan tacccggaaa 120
atttgctttt gtttttcct aatgctaatt agtgcaattg tacttgtttg tgcaaggagg 180
ttcttgtttg agaaattatt tttgtttgga aatatgtttt tataatttct tcaatgctga 240
ggaaaaggtc atttctgtag gtaggctttc ctaggaaatt tgtcccagca ggttgtgtgc 300
aggtggtttt tgcgggagaa ctctcaggca tgctacctat gaggggggtga agaaggagaa 360
atttggtaga gggaaaaaaa tctgaagctg ggatggccct tgagagatgc cttgacttga 420
gtcaagtgga cccagccttg ggacctgtac atcgttagga ggctgcctag ggcctgagaa 480
ataggtcaag actgctaact tcaaccaagg gcagtgtccg ggaggaatgc agggtgaaac 540
catctgtagg tagcactgcc aactggagga gtctgtgccc ccaggtccca agggtgtcat 600
tgatctgctt atgtgaccta ctgactctat ataaggcaaa gaaataatgg ccttagaagg 660
ctgcatgtcc ttgcttattc agaaatgcat ttgacagaga aaaaggcatc tgtcagaatt 720
caagtcagag aagaatgatg tagaaaaaag agctggaaaa ttttctaggc agtcccaacc 780
aaaaagacat tgttttatgg cataaatcca aaagaatcaa agaataggta aggagacaat 840
aatcaaaacc tcttagaaat tagaaagttg atgcatgcta acagatttgc tgaaacttag 900
aaaaagtaat atgaagtagc agagaggaaa cagagtcagt tcgatttaca tccagagtca 960
ggtattgaca acacgagatg caatggaaga aagagcaaaa taaggaagac tgggtggaag 1020
tcagttttaa gaggcagtca ggtccccaaa tcccattccc tactcccatc ccagagactg 1080
ggggcatatt tcttcctgga gggaactttt tctttttgag atgataaaga aaaggttggg 1140
ccgggcgcga tggctcacgc ctgtaatccc agcactttgg gaggccgagg cgggcagatc 1200
acgaggtcag gagatcgaga ccatcctggc taacacggtg aaaccccgtc tctactaaaa 1260
atataaaaaa ttagccgggc gtggcggcgg gcgcctgtag tcccagctac tcgggaggct 1320
gaggcaggag aatggcgtga acccgggagg cggagcttgc agtgagccga gatcgcgccg 1380
ctgcactcca gcctgggcga cagagcgaga ctccgtctca aaaaaaaaag aaaaagaaaa 1440
agaaaagatt gttgatctga gcaacagtag gaggagttca gggcgggggа ccactctgac 1500
caccaggatt ccatgcacaa ctccaccctg aagctgagac tcccccagcc acatcctgct 1560
tctccctcct gctccctggc cttctgcttc ctggatggat attggataga cttttctggg 1620
aagtctgatc aacctaaaga cagaatttca aaagttcctc catcctggcc gggcacggtg 1680
gctcaagcct gtattcccag cactctggga ggccgaggcg ggtggatcac gaggtcaaga 1740
gatcaagacc atcctggcca acatggtgaa accctgtctc tactaaaaat acaaaaaatt 1800
agccaggtgt gttggcggga gcctgtagtt ccagctactg gggaggctga ggcaggtgaa 1860
tcacttgaac ccgggaggca gagcttgcag tgagctgaga ttgcaccacc gagctccagc 1920
ctggcgacag agcgagactc tgtctcaaaa ataaataaat aaataaaaat aaaaataaaa 1980
gtttctccat tctaacagtt caggcatgtc atctcacgtg cagctcacag gccgcagccc 2040
tccttaggtg cccagacttc ctgtgcttgt tattttgtgc agacaactag gaatgcatgg 2100
tgtttccatg agaagaacaa gggacaaaca aacacaaaag ggtggcaaca cagagaaaat 2160
ggagggaatt tattcaggga gggaatgaaa cacaacaaat aagcgtaccc caaatatctc 2220
agagtgagaa aaacataaac atggtaacca taaaataaga acagttgctt cgaaaagcaa 2280
cattcggata acacaaagga gctcttggaa cttgatccta gggaaaaaag caaaattcag 2340
tgaaattatg tcacgtgaaa actcaccaaa ttccctgaaa gcagagttaa gggatgaagt 2400
aatatgaaat attaacagca gaggtaagaa aattaaagga caagttctga aggtccaaca 2460
gccaaacata ggaccagtgc ttgaataaat ctgaagaacg atcatttcta aattagaatt 2520
ccatacccag ccaaacaatc aattaaatat gaggtagaat aaacacactt taaggcatat 2580
ggcatcttgg aaattcgccc tcatgagctt ttcctactga agacactaga ggttgtaaac 2640
cctcaaaagg agaaagaagg ggatgaggca caggatacag ggaacagggg atccagcact 2700
gcagtgcacg gagcagtgga gactcatcag gcatgacggc aaccagtcca gatggtggga 2760
ggctgcagga gatatttctt cagaaaagaa ctgatagaac acttcatgca gctgaaagaa 2820
ctggcaatgc atttgggttg aatgagttag aagagggaaa ataacaagac aagtattatc 2880
tgtagaaaaa aaaacgaagt ggtataggga tagaaaattg gactttacta catggttgag 2940
ctaagaatta catttatgtc atccttatac tgtaaatgga acagcaggta tcaaagttac 3000
tatttatgga ggaatgggtg agggtttggg gggaagcatg tttgctggag ggaggaggag 3060
aataaatgtt ttatctccac acttcctgag gggaatctac agataatgct aaaaatgaaa 3120
aatcaagaag agcataaaac atgttattct cagaaatgca gctaaataca aagcagctga 3180
aagatatgca aatatttgcc tttgagaaag aagaatttga gatgtgggag gtggaggatt 3240
ttttttgtta ttttgtaaaa tactctgtgg aattatttta tcttaatata gatgcatgtt 3300
attcataaat ttgagtaaaa acttgttaaa aagatggaca ggagagaaaa aagaaagaat 3360
attaattgtg ccagacaaaa agaagggttc atttattggc ctgaatgaac tgcttccatt 3420
tttttttctg cgatgactgt agttgtagat cagcaaacca gtttctgagc aagtttggaa 3480
gagcttctta tttacctaac attgttaaat atattctgat tattagcatt ctaaaatgtt 3540

gatctaaagg acttctagat ttctattttt ataatcttat tgtaaactcc ttttgttgta 3600
gaatgtagta ttggaaacgt atatttcaat aaatgattag tctagcagtg agatatctta 3660
tatgaaaaaa gaaaatatca tacaataaaa atgtcagagc tgaagacctc attaattcag 3720
ttttttttta tattctacct aggcgaaggt gaagtttacc tttgaatgcc taagaagaaa 3780
tgaatattgt aagcatcatt ataaggatat cttgttcatt tctttaaaag aaaatgaaga 3840
ttgaagtgta tattatttga gattattttt aattaaataa ataggtatac tgagtttatt 3900
catgcaataa atgcttatta agtattctgc tcaggcattc tgctacatat tgggaataca 3960
aaactaagaa tgtatagttt atgcttttaa attgacagat aagtaagaaa attgaaatta 4020
aaatgagcaa ttgtgattac aagaaaaata agaataattg ctataattaa gagttaagca 4080
aaatgctaat agcccagggg tatgagtaca agcttcatac agggagtttc acttgaaccg 4140
catttgaagg ataaatgaga agtatgtaga ggaattggtg gaggacattt taggaagaaa 4200
cagtagcttg gcgagtgata caggcttggg tgctctggga agagccaatg cttcaggatt 4260
gcgggaacat tgagcagtga gcctggngag ngaggagaga cctttagatt ttattgttta 4320
ggttgaagca atgagatacc attgataact attgttattc acagcagccc aaattttcat 4380
gttatttcta tgtgctaggc actgaaccaa gcatgtgaca tgaaaaatct catgtaatcc 4440
ttacaacaac tcnnactatt atccccattt ttaagttttt catgcatgac attaatatga 4500
caaaantttg tgtagaaagn nttcattcta acacccatgg ataaatggtt cagtcaangt 4560
agaaaaaaaa tacactatgn acttatatag cttgcataaa aatattctat gtaatacagc 4620
aaggtaaagg attggaaaga ttgtagatac acagttgctt tattcttttc accacttcca 4680
aagttttaaa atatgcatct gtcaatttta aaataagaac aatgtgtgtt atcagaggaa 4740
gaagacaaaa agggaaggaa gagtttcagc aaggaggaag aaagtgaaga gagaacaaga 4800
gaagcggaga gagacagaca attcctgata ggcacaattg gaggacagat caaatgagaa 4860
gatgaacagc agagagactc cttctgtgat ggtcccagca aaagataatg aagcctcaac 4920
tgaggcagac ttctgtagaa agcaaatgga gaaaatggag aaaaataaga gaaatgttta 4980
gaaaataaat caaaatgacc cgatcaccca ctggacatat agatggtttt gcccattctc 5040
ccagagaggg ggagagaaga cttgatgagg cttctgagag gaaacgatga taacatggtt 5100
cctagagcta tgacgttatg atctgttgct tatttcactc agcataacta gctaatgtca 5160
gtttacgcag tgcatcaatt ggtcacattc ctgtgaaaga agaaaggatg actgcatgta 5220
cttgatatcc aagttgatcc ggaacctcaa gttctgattt tgacttaatg aaatcttcta 5280
ttctgtattc ccaacaaccc agaactttca tggtatgact ggcaggaata taaaagaaca 5340
acttgaggaa tctaacaata ctggtttgag accatgggtg actctttatc caattgcatt 5400
gacttgattt tcctttaaat aaatgtctaa ttgcctgtaa gattttgtgg gttagaatgt 5460
taaagcaaca gcttcactct actatgtcgc aaatgtattt ccttcctgct gacactctac 5520
ttccttcttc ctacagggct ttatgaaacc tttctaacca atgatgaacc agaatgctgt 5580
gacgtcagga gagaagaaaa atcaaataac ccatccaaag ggaccgtaga gaaaagtggc 5640
tcctgtcaca ggacatcgct cacagtgtca tcagcaacaa gactgtgcaa cagcagactc 5700
aagctgtgtg ttcttgtact gattctctta cacacagtgc tcacagcctc ggcagcacag 5760
aacacagccg gactgagctt tggaggcatc aacacgctgg aagaaaactc aaccaatgag 5820
gagtaacgga aggacgagtg tcaccacagc agcagctggc ccgccgtgaa aaatggcaac 5880
tgctgtctca tgtaacagaa actgggtgct tttaccctcg aattacttat tgcaaggcct 5940
ttagggtaaa atttaaanca gatgggcctg aatccaaaca aggacacaac cacagctttt 6000
tattgactaa aaggctggaa agtgacttta aatttctcac accattttat acactgtgtt 6060
ttaatgtttg gaggttttat ttgctttcgt tttggtttgg gtttatttgt ttgtttattt 6120
tttgcacttg ttaatacagg atttattttg ggggatggtt tctcagaggt aaactaagtc 6180
ttttcactgt ctctatctct ctatatattt ctagtcattg tgtgtgttca tcagatagtt 6240
ctgtctttat gtcctgtcag cttctattag aggaatgatt gctatgacct catggtatag 6300
caaaaaacaa caacaaaaaa agaataaaaa ataaaaaaga caaaaaaaag aaaacaacaa 6360
aaaataaaaa taaaaaaaat ccctaagtct cccttctacc cacagaacca acaacaccct 6420
tcccagcctt tcctttccct cgccctcttc tcgtccccta agcaaacaac atccgcttgc 6480
ttctgtctgt gtaaccacag tgaatgggtg tgcacgcttg gtgggcctct gagcccctgt 6540
tgcacaaacc agaaacagag cagagccaag ggggcctgac aagagttcct ttttagctga 6600
acaaacaagt gctctccata ataggtggaa tcagacagtt aacacatttt tatgttgaaa 6660
acaaaataaa aggaaaaaat taaaaaaaac tatcatgaac tgtattgctc cagttcccat 6720
ccccaagtgg cccagccctt tcttgctggt ccagctggac aggagcagct atctagaatc 6780
aggatgcggg gagtgaggaa gtttttcctt tgacaatgaa ggtgggcttt cattgtgatt 6840
tttgttctgt tgcagtaata taggagcaca ttttggccat tgtaattaca gggaacaaag 6900
ggattgcgga cacatatctg gacttctttt cctcccttat tgttgtggaa gagacactag 6960
aaatgctcaa acacctgcaa tatacagaat atacacaatt ttattccagt atttccctaa 7020

catatggttt aaaattattc caggtataca gtgtatgcaa ttctgcatta tcacagagga 7080
acaacttctt ttttaaaaaa taaataggtc agccattttt attaacgtgc aaaaacttta 7140
tcactctaac atgctctagg tagttgagga aaagaggtct gatcactgtt tgtattttat 7200
tttctttgtg ggaacatttc acctgctgag tgtacatgaa tttgctttct ataaaaggct 7260
tttatgagtt tacagtagaa tcagtggaag gaagagttaa taagggctgt ttttaaaaaa 7320
acaaacaaac aaacaaaaca aataattaaa aaaaaatttt acattccttc ctattctcta 7380
actacacttg ggaagtgcac ttcagataag tttgcagtgt gactgagaga tgaaggaaat 7440
ccatagaaaa ggtcctctta gtgaacaaaa tttagttatt aactttatag ctatgaaatt 7500
tccccgggca tttgtttttg ttcaaacaga ctttaacctc tgcatcatac ttaaccctgc 7560
gacatgcgta cagtatgcat attttgtttt gaaaaaaaat gtttcgttcc agtctgttaa 7620
gaatattcaa aaataataaa ggtattgctt aataaaattg ctagaattgt ttagcagtac 7680
atgcacaata ttttactaga ttctttgttt taatagtgtt ttgttgagac tgaaaatctt 7740
aaaatggtct gcgcaaatac aaaaaaaaag aaaacaccaa aaatgcaaaa ttctcccgtt 7800
tttgttcctt tttaaaaatt tttttttctg caaatgcaaa tacattcaca tgtggacaga 7860
tacatacaca taggcatcat attttagtgt atggaaacat ggtgcttttc tggggacaca 7920
agctgaggaa gtgaatggct cgggggagac acattaattg catggaattg ttgactgtga 7980
aacacttgta gaaatgagca ctttggtatc ccaaccaatg gtggaataca gatttcaatg 8040
gcgctggggg gacgagaagc agaggaattg aggctgcaag tgattcctga ggaagagctc 8100
acagggtgat tttattcaga tgacctctaa gggaatggct aggaaggagt ctgttctgac 8160
ctttatctac ctctgctgtg gtaaggccac tccatgtgcc atctcaccat ctcttcagcg 8220
ttcctcatgc tgcttctccc cgtgccatag gcgtttccat tcttgcagga aaatgayaat 8280
gcaagtgcaa attccactca cttttattgg tatgacaata aattattctt tctaaacact 8340
tagcaaaatg acgaaaagca gtattcctta aaatataggt tttcattttc tcaatatatt 8400
ttgaactgac taaagttctt tacaaagaca agaggatcag aaggttccac ttacccgtgt 8460
tttagcgttt gtttgaagat aatgccaacc aaaaggtgga aaactaaaac caccattgct 8520
ttacataaga ggtacacact gccccccacc cccaaaaaaa aacacagctt tgaaagttgg 8580
gagaaacact gcagtcttca ttgtaaatat aaagtgataa tttaggtgag gaaggaacgg 8640
taaggaggga aggggaatga gtcctttctc cccatcaagt cagccagcat tggaatagtc 8700
tctaattctg gcggaatatt ttctttgtca tgttcatcta ttcttattac aggagaatga 8760
tttcagtgcc tagtatttat tagtgtaagt gtgtaaccac tttcccgcaa tatttccact 8820
ggacatgttg aagcaaagca gcttcttctg gggtcaggca gaggatccaa ataggcaacg 8880
actcctttcc caagctcaga aacaatcact gatgatgcag atttcactac atccgttgat 8940
tctttgtagt agttttcctg gcacacactt gagcatgctt aaggttgtgc atatgttcat 9000
tttgaacaaa taagttcagc ccctgctcct ttgtaatcat catcttgttt agtttttcct 9060
gtagaggatg tctaccgtat actggctaat gaactacaat attaaaataa ttatttctgc 9120
aagcaagttg aaaaccaaga aaacaatatt tgtttcataa atgtatggca tagatttccc 9180
tgtttattat tctttttatc tgcaatagag aaatttcagt ttctggaata tgttggtact 9240
gctaagctaa atggcaaata acatagagtt caatgtcatt ctttattgca tttacatttg 9300
gtgatacgtt atattgaact tttcttgcat taaaaagata gtatttttcc cctctctcac 9360
aaggcagtaa gtgaaagttg ttcttttaaa tggcatcatt acaaaaagta atttggtttc 9420
ttaccaataa attggtacct taggtactag aacctgtagt cattaaaaca aaagaaaata 9480
ggcagatagc agaaacaaaa gaatgacagg aaagaaggaa ggaaagaggg gagtgaggga 9540
gggagggaag aagggaggga tagagtcagg gaatgagggg gaaaggaggt ttcatatgaa 9600
tgaataagta catacttttt tccgggggaa aaaaacataa atgaaataag caattggatg 9660
ccagacccat gtgccaaata cctgaattgg catatggtat ttgatatctg aacaacatca 9720
aaaacgttaa ccagtctgaa gcatgattta cattctttct cagtaacaaa gacatttaca 9780
attttcctgc tactcaaagc attaaatcaa cacagaactg aaagctgcat tttgttttat 9840
ttatttagaa ctgcagtcag gtatttaatt tcttttctgt gtgtttgttt gtttttgag 9900
atggcatctt gctctgttgc tcaagctgga atgcagcggc aagatctctg ctcactgcaa 9960
cctccacttc ctgggttcaa gcgattctcc tgcctcaagc ctctcgagta gctgggacta 10020
caggcttgtg ccaccacgcc tggctaattt gtgtattttt agtagagacg tggtgtcgcc 10080
atgttggcca ggctagtctt gaactcctga ccttgggaga tccgccgatt aggcctccca 10140
aagtgttggg attacaggcg tgagatacca cacccagcca ggtatttaat ttcataagtg 10200
tgcatatgca tatatgaggc gttagggtta tatactatgg catatcttta gagagatata 10260
aagatatata tacatacaca cacacacaca cacacacaca cacacacaca tcgcttgcaa 10320
ataaaacttc aaccaaaaca ttatgtagtc cataacagca catgtatacc ataatgatga 10380
atgatcctac ttgtttgtca aagttagagc agcatggtca tttaaaaacc atatctactt 10440
tgacaaggga aacagactct caaaatatct ccattaatga ataaatcaca attttgaaac 10500

aggcagaatc tccatcttcc aagctttaac aatgtttata aaaaacctaa tatagcaggt 10560
aggtattggg tgacaatgaa taaaaagact ttcagtgggg gggaaggaaa ataactaagt 10620
atagttttca agcaatgtct tcatgacatt tataagaact atcaaacagc tacaaattct 10680
agaaattctc caaataatga gaaaatgtat agataatctt cttagccttg gaataaaact 10740
taaggcatga aacaaaatat gaactatggt ttttattctt gagatactgt acttcagggc 10800
tatgtttacc acagacaaga cattcagatt aaactcagaa gaaaatcacc tggttatttt 10860
gtcctgggtc acacaggtag gtaatgcaaa tgatggaact caagcatctt ctgattacaa 10920
attacacaag ctggctccga ggcacagtgg gatccctagg tctcagacac acttgaagag 10980
ttgaatggat tttcttcata ctccaagata tttgtagaat cactcaatct taaatgaaaa 11040
aatcaaaatg atcaggaaga tctagcgaat gtctcagagt tcgtttgtca tgttacattt 11100
tgttccatga ctttgctgtg ttattcaata ttttggaggt aaaggagaag agggtctatg 11160
ggaatatttt aataaaatat agatttttaa tttttatttt taatgtggag aaaaggcaca 11220
ggatcttagg gcaaagccat ggtttaggga tgagctttgg ctccaggtga cacagggagg 11280
tcaatgatgt atttgtacgt gacacctcat gcaagaagaa tacttcgtgg caacattgga 11340
ggcttaaaag agataagtaa tataaatgtg cctggacaaa acaggtgctc agtagtagtt 11400
agttatcatg actattcatt cacaaagtga aactggattg gcttgctcat agggactgct 11460
cctggaagtt gttcagagtt tctgaatttc tttggcttat ctcttaatta catttttttt 11520
ttaacaacac ctcacatcct taagctagca gactgaccat caatagattt tcaatacagt 11580
ttgaaagtct taacatatat tacagaacta aagtgagctc tgatgacttt taatataaac 11640
agcattggct attttcgatt tccactccca aaaggctact actgacaagc aaaagttaaa 11700
ggcatctaca caaattgaag tggttctaca agcaagtgta aattgatcaa cagtggtagt 11760
agaaataatg atgcaacttc aaagtggttg tttaaggcac tcatagatca aaaaatatat 11820
ataaatattt gatgcctctg aattccttaa aaaaactata gtaattttaa acatgaaaat 11880
gtttaaattg gaacatttat tatgaaaatt aattaaactg aattaatata tattttaatt 11940
aacactataa ttattataga atgaaataac agtgaaaaag ttagaaaacc tgttcagttt 12000
ttgataaagt atatggaaat agattaagca gggctcttga gtaaattatt tcattgattt 12060
gtatctattt aggtaggtga gagttgcata gaatcagtgg cgagaaggat cagtgaaata 12120
aatttacaac ttcagtgaag accaggtaat gagcattgat ctatgaatac agactttctt 12180
cagtgactat ttcccctaaa actcccagct caccgcagca ctgctgcttc aagattccag 12240
ttattggcgt gctagccaag tagaaggtca tttttaccga aacgcaaatt tcaacttatg 12300
gccatttttct actgaccatt tcactgcaaa atggataaaa caataggaaa tataaactac 12360
agcaaaagtt aaagctctat atggacgtta aaagaaaacc tcttgctttc tttttcttcc 12420
tttttctctt gttttctttt tctacctttt tctgcatatg gcatttattt tcatatcatg 12480
ataagcattc tcatgtttgc acttaatttt ccttatttct atttttctta gatttgttga 12540
tgttgtgtgg catattaaaa gtaggaagga ctgtataaac tcatgtatta tttttaaatt 12600
gtttttctga atgtactcaa gtacttttt atgtgaatat gaacacggaa taaaagtact 12660
aaaaccagtt aattatgaga gactaagaat gtggaaagga acattccgga gtatattagt 12720
agctaaagaa atgccttgga tcttaaattt caacttctaa aattattaaa atacaaatat 12780
taaaaagata tagaggccac tgctaaagtt tgtttacgcc ttatttcttc ggttgcctag 12840
attattcgtt ttaggtgaat ttgctttttc tgtcaccgtg gttatgttaa cccaactgat 12900
tcatccaaaa cggaattggc taaactcctt tatgcacata tttatattag ggctgattat 12960
tttgctcatt gagtttcaaa aaattatcta gaggactgcg aagttttcat tgctttactt 13020
aatttctttt tcgcttgtgt gatttttatt tcttactctt gactatatct ctatacggtt 13080
tgaagtaaca gggcagaaag ttaagctaat aatttctgct gacttgataa ttcatcagtt 13140
tgacaaaaag accagtgggc caccattagg aactgaaggc aactgaaatg acatggctta 13200
ctcttgctgg aatcttagct tgaaagttga acatctactc cacaatgcca cgggatccgt 13260
tcatgatatc atttgctgaa gcacttgcca agaatttcat tatttagaaa aagcagaatt 13320
aacatttcta tctattattt ttcttttctt tctttaagct gaaaggcatt cagaggctgt 13380
cagtaaataa aatctatcag gaacaaaatc attttcaaaa tttttaaaca tgatttattc 13440
ttgatgcaaa tcttattgtt cttacaattc tatgcaagtc aagttgagct aaagcatttt 13500
tatttaattc aattttcttt cttctgaaat gtgatacagt aaaatcaggt tttgaatatg 13560
tacaaacaca tcaggatgat tattatactt acataagtaa aatatatgta aaatattatc 13620
atatcttcac catatttaga gtctaatatt tgttagattt tttgtgtgtg cattttttct 13680
ttccccttca gaaaacgtag ttttttattt aattcatgtg gtttttctat agctttctgg 13740
gtctcatcaa atttcacatg aaactatgca gagtcatatt tatgttaagg aagacatgca 13800
attaaaaccc tacccatttg ttttgttagt cccaacacgt atcaaacaaa aaacttatgt 13860
tgttagatgt agatttgatt atctcccttt atttatttgg gtctctctct ctctctctct 13920
ccccgcccca ccgtctgtct cactctcact ctctctctct cactttctct ctgatctctt 13980

ttcctttcaa ctcagcttgc aggaatggat ctcatttgaa atgagctgca ctggtgtcag 14040
catggttgtt taaccatgta aactatctca tgatgcttag aattgaagag aagcttaaac 14100
gcttgtgtca gaaaaatatc ttacaataca caaaacacat taaatatatt attagaaaaa 14160
gtttagttgt gcaacaaaga cctttaattt caactaaaaa ctgatgcagt aatgtattac 14220
aatgacccaa aaagaaatat tcttttcaaa atgacttcgg gaagctatca gagtttgtgg 14280
gaaaaatgct aaggtaatac tttcctaaga acaaatgtaa agctgcaaac aatgactttg 14340
aatttttcaa gattagcagt ttggatttac atgtatttta acaaaatata aaaaatttac 14400
tttcaaatct tggctttaaa aaaaaatcgt gtggctcatg cctgtaatcc cagcactttg 14460
ggaggctgag gagggcggat cccaaggtca ggagactgag accatcctgg ctaacacggt 14520
gaaaccccgt ctttactaaa aatacaaaaa attagctggg cgtggtggcg ggcgcctgta 14580
gtcccagcta ctcgggaggc tgaggcagga gaatggcgtg agcctgggag gcagagcttg 14640
cagtgagccg agatcgcgcc actgcactcc agcctgggca acagagcgag actacgtctc 14700
aaaaaaaaaa aaaaaaaatc atgtttcaac tgaaatggat atttattatc tgcaaaagtc 14760
cattttgttg catatattgt ttaaaataat tcttaagaaa ttgttacctt tctatttcta 14820
tggagaacta acaccttaat acaagtctag ccccctttc caagacacaa cgtcccccac 14880
aatgccactg agtttgtgtt tacctgaata ctttcaaacg acagctgatc cttgaataac 14940
atgggtttga actgcatgag ttctcttcta tgaagatttt ctttacctct gccatccctg 15000
agacagcaaa accaacccct cctcatcttc ctccttcaaa gcctactcaa catttgaaga 15060
tgatgaagac gaaggccttc atgatgactt catatgactt tcccttaata aatagtaaat 15120
atacttttcc ttccttatgt ttttttatac cattttctct tctctagctt actttattgt 15180
gagaacacaa tttataagca tataaaaggc agtatagcaa gatcccatct ctaaaaacaa 15240
atattaaaaa aaaaattagc ttggcagagg ggcaggcact tgtggtccca gctaacagag 15300
aggctgaggt gggaagattc cttgagccca gaagtctgag attgcagtga tggcaccact 15360
gcactccagc ctaggtgacc gtatgtcttc attgattatt tctgttatca gtaaggcatc 15420
tagtcaacag caggctatta gtggttaagt tttgggggag tcaaaattat acatgaattt 15480
tcaactgttc agaggtcaga gcccctaact cccagatttt tcaaggacta tctgtatata 15540
caattgtagc actgctgcta taaatgtgca gatatgtttt aaatgatcta aggctaacaa 15600
aaacatattc agcagttttt ttaattttaa gaataatcta ttcagaatgt gtatccctgt 15660
gcaattaatt acaaatagct aaaatcttgc aaaatattta atgtatcaaa tcagcatgtg 15720
atttcattta tagaaataaa agactagttt tctcccttct tttacccatg aacttggcta 15780
attaattttc tatttttccc tcaaactttt ctcaaaggtg ggtatgaagg gaaaacttgt 15840
ttttgtgaca ctagagagaa attgatgaag cctgggcaca acgtcatttg tctccctgtc 15900
acaaagttgc aggtragctg gccattcatc acctggtaca cagcacacct catcttgacc 15960
aaagagcacc tttcttcatc agagaagctg tgctattgag agcactggga accaggtctg 16020
aattggaaca agaggcagaa aagcagaatg atrtttcttt ctaaaatcat ataataaaca 16080
ccaataaaat ttctgaatag tagtaacgtg tcttttgtta ttcaaagtag tattatatag 16140
cttttcctct tcatttttatt gaaagtttca ggaaggggga atgtactaaa gcttaaaatt 16200
aatatctaat gcttttcatc ttgagaacag tatgtacatc ttgcacaact atattttagt 16260
ttgtataaaa tagacatata aattacctgc attcatggct ttcattcatt tatctgaata 16320
aacttactga gcagcctcta tgttcctggg actgggcaag gcattggaga aatagataca 16380
aaagacctat ttttggactt ccaggggttc ttagaccact gtggaaaaag ggcatacgat 16440
tacaatgcat gttatgtaaa aaatatggca aagttagagt acactggaag catttaactc 16500
ctattgacag aagttagttg cacaaataga gtggcatttt aaatttaata atcagatcta 16560
aattcagcca gcaaaagaca cagaaatttt gtcatgtgca aagatgggaa atatcaaaat 16620
agaaagttgg gggaagagtc actttataaa acaaatgatt acctttagat tgaaagaaag 16680
tcatgacccc tattgaaaac agacagacaa atgtcggtat aggatctgtt gaggaacaga 16740
gggagtaaca gtggggaatg cctcaatgct attttgcctt tcagcagaga tgggcagaag 16800
agatttgaaa aagggttcat ttttatagat gtatgtaggt atttgtatac gtgtgtatgt 16860
gagttcaccc acacatgtat gtatgtgtat taataaccca ctgacctcaa agtaagagag 16920
aaataggatt tacccagtat ttacccaaga atccccatca tccttatccc aggattctgc 16980
agtcagcaaa ccaggctttt taacactctc caatcatgag gtatttaaag arctccatga 17040
tttgttttgt atttaacgct gcaataacca ttctcagata aacatgtttg agggcttctt 17100
gagatacatt tttctaagga aagtttatgg gttaatagag ctttaattgt tttgggtata 17160
tatttccaat tttccctacc aacatttntg caaaaggcac agagcaatcc agctgtacac 17220
atgcatgcct gctgcatttt catagaaagt tcttcctacc atgaaaacat acctttttact 17280
cagttctctg aactgtggat ttcacgtcag gagagtaaaa atgtggnngt agttatgttc 17340
ttggttttct ttgggagtgg gttcttgagg aaagagatga caaacaagaa taggcaactt 17400
caggtctcca aaccncagaa ttggcaaata tagctaaacc ggaaggggac agtcattttc 17460

aagtgctgtg ttttttaaa atatcaggta atttttaaaa tctacgttta atataacttt 17520
atcagcaatc aaaaaaaaaa ctggtcaact tgaatgatct tagtcgtctt ttctatgagg 17580
atctcttctt gatgtaaaat atccaaaggc cctgttcaca ccttaggaca ccagttagca 17640
ttcgtttctg ttgatcaaga aatatatata cagatgctct ttgacttaca atgaggcgcc 17700
atcctgataa acccataata agttgaaaat attccaagta aaacgtgcat ttggtacaag 17760
tacacctaac ctactgaaca tcatagttag tcctgcctac ctgaaacgtg cttggaacac 17820
ttacattagc ctacagttga gcaaaatcat ctcacacaaa accaattttt ttttttgaga 17880
tgtagtttca ctcttgttgc ccaggctaga gtgcagnggc acaatctcag ctccctgcaa 17940
cctntgcctc ctgagttcaa gngattctcc tgcctnaacc tcccaaatag ctgggattac 18000
aggcatgtgc caccacaccc agctaattct gtatttttag tagagatggg gtttcaccgt 18060
gtttgtcaga caaaacctat tttatagtga agtgtcgaat atctcattta atttattgat 18120
gttctactga gtgtatatca cttttaaacc atcgaaaagt ttaaaatcat taagtcaaac 18180
ataatctgtc aaaccattat agtcgaggac catctctaat ctgnaatatg aaacattaca 18240
ttacatattt atgtatcata taatacttca attatataaa atgaatttac atatgaatcg 18300
aaatagtatc cacacatatt taacaatata tgtacatata tttcatttca catagtgtag 18360
acccctagaa attaggtcat tgtctgccta ctccaaatat catctaaata ccatccaaag 18420
gttgaaaatt agttcctcaa ttatgttaac atttcagtgg aaacattaaa atggtagtaa 18480
ccataagctt gccattaatc cagtaatgac atcagatttt tgaagattta tgttcaattt 18540
cagacttcat attttaaaag atatgagcta tgagaacatg acaatgatta aaactttaca 18600
aaataaaata tctggggaga aaggaataat attgggatat attactgaga aggaaaagaa 18660
ggtgaaagag agacaactta tttttcaggc atctgtcaga gccaagaact ttggataaat 18720
tatttctggc tctcacaaca aacttgcata aaaggttttt taatcctaaa tttttggagg 18780
agatacaaat ctctgagaga gtatgaaaat gagtcagagt cccataaatc gggaacatct 18840
gttcttggtc tcaaacccca tgccaggacc atgttctttc gataacaaca cacttaatac 18900
agtcctgctc tcctaatcag gaaagacaca agggtctatg aaatcactta aaattcaaga 18960
tttagcctta attagtaaaa agaaattgca aatttaattg tcagaaatgt ggaagaaatg 19020
caataacatt gtttaggttt atattcctca aacctttggc ctcagaataa agggttaggt 19080
tccgtattgg ttaaggatga tcatatcaca tttatataaa atcgctaaca aaatcagtca 19140
atattaactg aaaaatggtg ttcaggacaa tggtcaagat gaataataga cactaactcc 19200
tattttgaca agtttataaa ttagttaagg atacaggcac atggcttaaa gacaattggc 19260
agcacacttt tcatcccatg ttctcattct gttgttggca aataacaaat tatctttgtg 19320
tccagtgatt tagtgatggg aaatcattct cttaaacttg ataaagaaaa ttactgttct 19380
ccagaaaaaa atatttcaag rgagagaata tcagtgatgt aatgagaact tataaatgta 19440
aggaatgcct cattataaac atagtattat atccagctca gtgtcaacaa tggtaatttg 19500
tggaggaggt tagcgattct ccatgaactc gacccaatgt cataaacact catttctcaa 19560
gaaaacattt aatttaagga accctcagtc tgctttttag caagatatgt agtttgaata 19620
ataatattct ggtttgaact gttttaaact taggcacact gggtagttgg cctctccatg 19680
accaactggc tttaggcatt gtgctcactt tctgtgagat ggcagtaagg gataaaactg 19740
catcctgcca gcatacagag gattctggat atcatgggct atccntggct tttagcctgc 19800
tttctggaaa taagccaaaa ataagtatct ttataaggcc tgctaggttt tatgtgcaga 19860
aattctaaat aattttcatt atgaaatata gtaaggagag gccgggcatg gtggctcacg 19920
actgtaatcc cagcatttgg ggaggccaag gtgggtggat catgtgaggt caggagttcg 19980
agaccagcct ggccaacatg gcaaaacccc atcgctgctg aaaataaaaa aaaaaaatta 20040
gctgaacaca gtggcaggtg cctgtagttc cagctgttcg gganactgag gctggaaaat 20100
tgcttgaaac tgggaggtgg aggttgcagt gagctganat ggcatcgttg tactccagcc 20160
taggtgacag agtgagactc tatctcaaaa atgaaaagag agagagagaa agaaagagaa 20220
ggaaagaaag aaagaaagaa ggaaggaagg aaggaaggaa ggaaggaagg aaggaacaaa 20280
gaagaaagaa agtgttgaat aaacttgtat ttagattgtc taggattatc tatataaggt 20340
caaactcaat ttccagatta atattaatct attcccactt aataaaatgt ctctatttct 20400
atatacactt aagagaccag ggattttgct gatggtaatt taaatttata tagtgaggtt 20460
tacattttga aattaataac aatttttttat tagcattaga gacttaattg tttaaagcaa 20520
tcttacctac ctactatatc agtagctaac tgctgcctac cacagcagtc acacaacagc 20580
atgagcacaa aatgtttaca gttaccatgt ccctgcccag agggtatcca aaaattacat 20640
tggcactaca gctaaataaa cccatgtaaa acatatacta taaaagagtg tagacatata 20700
tcacattttt atggaaagta aaacattgcc taattttaga taacaaaagg aaaattgtta 20760
tctacacaat aaatgaatta aaattctcat ttgtcataaa acagaaagga gagaaaatca 20820
ggtcacttgt ttactagtca aaattatcag aattcaccca aatatgtagt gtgatacttc 20880
taaatacaat aatatagaga gaaatatgag ccaattacaa tcatttttat ttagagtact 20940

agttatttta atgaaattta tttattgata atggaaaact ttttatttt tattttatgt 21000
tacttcaaaa taattattaa cttacggaat agcttcaaga acagtataat agacttttc 21060
ctgttttccc aaaccatatt ataataaatt gtcaacctga agcctgatca ttcagaatat 21120
cttaagtata catttcataa aataaaagca ttctccttta tatcgatgat acagtattaa 21180
aaaacagaaa gttatactga tattactacc atctagtcct cagatcctat ccaactttca 21240
ctcattatcc caaaaaataa ccttgagagc aaaagaaccc aatttataat tacatgttgc 21300
attgagttgc cttgtctctt ctgtctcctt cagtctgaaa cagttcctca gtgtgtattt 21360
tactttaata gccttgaaac tttggatggt tacaggccag ttacatttta gaangcctcc 21420
tgatctgnct tgnctgatat ttccatatta ttagcttgag gtnacacatc tttgctaaan 21480
tatcagaaat gtttacccta tcatgtaaaa cattatttta ccctgttcca gtaatgatga 21540
ccttcacttt aattgcatga atgaagtggt agcctcatgc ctggggatac cacacacaca 21600
cacacacaca cacacacaca cacacacaca cacaca 21636

<210> 4
<211> 5566
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 659..2032

<220>
<221> allele
<222> 4484
<223> 99-13821-332 : polymorphic base C or T

<220>
<221> polyA_signal
<222> 2531..2536
<223> potential

<220>
<221> polyA_signal
<222> 2538..2543
<223> potential

<220>
<221> polyA_signal
<222> 2873..2878
<223> potential

<220>
<221> polyA_signal
<222> 3307..3312
<223> potential

<220>
<221> polyA_signal
<222> 3843..3848
<223> potential

<220>
<221> polyA_signal
<222> 3859..3864
<223> potential

<220>

<221> polyA_signal
<222> 4524..4529
<223> potential

<220>
<221> polyA_signal
<222> 5536..5541
<223> ATTAAA

<220>
<221> misc_feature
<222> 10,39,2574,2580,2978,4692,4696,5466
<223> n=a, g, c or t

<400> 4
ggcagcccan gctccggact ctgggagagc cagcgcggna gcaggagcgg gaggcggagg 60
agaagaagaa ggagaaggaa aggaaggagg aggaagagga ggagaagaag aggaggagga 120
ggaggaggag gggaggcgct ccgggcgccg tcagtgggca gcggaggcgc ggcatgcccc 180
tggcagggga gagcgggctg ggctccgcgg ggccatgggg acccgcgcgc tgacaatgcc 240
tgggtggccg gagccgcgcc agccaccctg tcacctccac catcgccccc tgcacccagc 300
ctcgccgccg gccaccagca ccagcctcct ccgtctctct ctctctctct ctctccatta 360
ttgtttccca ctctacagag gatggggtcg gctgatgatt aggaagcaag tcagaccttc 420
cttcaaagcc tggtaatatt tatgtaggca aaagagacag agagagataa aagagaggga 480
gagggagaga gagagagagg agagagggag aggggaagag agagaaagag agagaggaga 540
gagaaaaaac gggaggaggg gataaggaaa ttaaaccctt taagtcaatg catattgtgg 600
tgacaccggc acaggcgccc tcacggtgga gtcggccagg gctgtgcgtt cccaaaat 658
atg acc agg ggt gct tgg atg tgt cgg cag tat gac gac ggc tta aaa 706
Met Thr Arg Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys
1 5 10 15
atc tgg ttg gca gca ccc cga gag aac gag aaa ccg ttc atc gat tcc 754
Ile Trp Leu Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser
20 25 30
gag agg gct cag aaa tgg cga ctg tct ctg gca tct ctc ttg ttt ttc 802
Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
35 40 45
aca gtc ctg ctc tct gat cac ttg tgg ttc tgc gcc gag gcc aag ctg 850
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
50 55 60
acc cgg gcc cgg gac aag gag cac cag cag cag cag cgg cag cag cag 898
Thr Arg Ala Arg Asp Lys Glu His Gln Gln Gln Gln Arg Gln Gln Gln
65 70 75 80
cag cag cag cag cag cag agg cag cgg cag cag cag cag cag cag cgg 946
Gln Gln Gln Gln Gln Gln Arg Gln Arg Gln Gln Gln Gln Gln Gln Arg
85 90 95
cgg cag cag gag ccc tcc tgg ccc gcg ctc ctg gcg agc atg ggg gag 994
Arg Gln Gln Glu Pro Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu
100 105 110
tcc tcg ccc gcc gcc cag gca cac aga ctc ctc tcc gcc tcc tcg tcc 1042
Ser Ser Pro Ala Ala Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser
115 120 125
ccc acc ctg ccc ccc tcc ccg gga gac ggc ggc ggc ggc ggc ggc aag 1090
Pro Thr Leu Pro Pro Ser Pro Gly Asp Gly Gly Gly Gly Gly Gly Lys
130 135 140
ggc aac cga ggc aaa gac gac cgg ggc aag gct ctt ttt cta gga aac 1138
Gly Asn Arg Gly Lys Asp Asp Arg Gly Lys Ala Leu Phe Leu Gly Asn
145 150 155 160
tct gcc aag ccc gtg tgg cgc ctg gag act tgt tac ccc cag ggc gcg 1186
Ser Ala Lys Pro Val Trp Arg Leu Glu Thr Cys Tyr Pro Gln Gly Ala

```
                  165                 170                 175
tcc tcg ggc cag tgc ttc acg gtg gag aat gcg gac gcg gtg tgc gcc      1234
Ser Ser Gly Gln Cys Phe Thr Val Glu Asn Ala Asp Ala Val Cys Ala
            180                 185                 190
agg aac tgg agt cgg ggg gcg gcc ggg ggg gac ggg cag gag gtg agg      1282
Arg Asn Trp Ser Arg Gly Ala Ala Gly Gly Asp Gly Gln Glu Val Arg
        195                 200                 205
agc aag cat ccc act ccg ctc tgg aac ttg tcg gat ttt tac ctt tcg      1330
Ser Lys His Pro Thr Pro Leu Trp Asn Leu Ser Asp Phe Tyr Leu Ser
    210                 215                 220
ttt tgt aat tcc tac aca ctt tgg gag ttg ttc tcg ggg ttg tcc agt      1378
Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu Phe Ser Gly Leu Ser Ser
225                 230                 235                 240
ccc aac act ttg aac tgc agt ctg gat gtg gtg ctc aag gaa ggc ggc      1426
Pro Asn Thr Leu Asn Cys Ser Leu Asp Val Val Leu Lys Glu Gly Gly
                245                 250                 255
gag atg acc act tgc agg cag tgc gtc gag gct tac cag gac tat gac      1474
Glu Met Thr Thr Cys Arg Gln Cys Val Glu Ala Tyr Gln Asp Tyr Asp
            260                 265                 270
cac cat gct cag gag aaa tac gaa gag ttt gaa agc gtg ctc cac aaa      1522
His His Ala Gln Glu Lys Tyr Glu Glu Phe Glu Ser Val Leu His Lys
        275                 280                 285
tat tta cag tcg gag gag tac tcg gtg aaa tcc tgt cct gaa gac tgt      1570
Tyr Leu Gln Ser Glu Glu Tyr Ser Val Lys Ser Cys Pro Glu Asp Cys
    290                 295                 300
aag att gtc tac aaa gcc tgg ctc tgt tcc cag tat ttt gaa gtc aca      1618
Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser Gln Tyr Phe Glu Val Thr
305                 310                 315                 320
cag ttt aac tgc aga aag aca att cct tgc aag caa tac tgt ttg gag      1666
Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys Lys Gln Tyr Cys Leu Glu
                325                 330                 335
gtt cag acg agg tgt cca ttt ata ttg ccc gac aat gat gaa gtc atc      1714
Val Gln Thr Arg Cys Pro Phe Ile Leu Pro Asp Asn Asp Glu Val Ile
            340                 345                 350
tac gga ggc ctc tcc agt ttc atc tgt aca ggg ctt tat gaa acc ttt      1762
Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr Gly Leu Tyr Glu Thr Phe
        355                 360                 365
cta acc aat gat gaa cca gaa tgc tgt gac gtc agg aga gaa gaa aaa      1810
Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp Val Arg Arg Glu Glu Lys
    370                 375                 380
tca aat aac cca tcc aaa ggg acc gta gag aaa agt ggc tcc tgt cac      1858
Ser Asn Asn Pro Ser Lys Gly Thr Val Glu Lys Ser Gly Ser Cys His
385                 390                 395                 400
agg aca tcg ctc aca gtg tca tca gca aca aga ctg tgc aac agc aga      1906
Arg Thr Ser Leu Thr Val Ser Ser Ala Thr Arg Leu Cys Asn Ser Arg
                405                 410                 415
ctc aag ctg tgt gtt ctt gta ctg att ctc tta cac aca gtg ctc aca      1954
Leu Lys Leu Cys Val Leu Val Leu Ile Leu Leu His Thr Val Leu Thr
            420                 425                 430
gcc tcg gca gca cag aac aca gcc gga ctg agc ttt gga ggc atc aac      2002
Ala Ser Ala Ala Gln Asn Thr Ala Gly Leu Ser Phe Gly Gly Ile Asn
        435                 440                 445
acg ctg gaa gaa aac tca acc aat gag gag taa cggaaggacg agtgtcacca    2055
Thr Leu Glu Glu Asn Ser Thr Asn Glu Glu  *
    450                 455
cagcagcagc tggcccgccg tgaaaaatgg caactgctgt ctcatgtaac agaaactggg    2115
tgcttttacc ctcgaattac ttattgcaag gcctttaggg taaaatttaa acagatgggc    2175
ctgaatccaa acaaggacac aaccacagct ttttattgac taaaaggctg gaaagtgact    2235
```

ttaaatttct cacaccattt tatacactgt gttttaatgt ttggaggttt tatttgcttt 2295
cgttttggtt tgggtttatt tgtttgttta ttttttgcac ttgttaatac aggatttatt 2355
ttgggggatg gtttctcaga ggtaaactaa gtcttttcac tgtctctatc tctctatata 2415
tttctagtca ttgtgtgtgt tcatcagata gttctgtctt tatgtcctgt cagcttctat 2475
tagaggaatg attgctatga cctcatggta tagcaaaaaa caacaacaaa aaaagaataa 2535
aaaataaaaa agacaaaaaa aagaaaacaa caaaaaatna aaatnaaaaa aatccctaag 2595
tctcccttct acccacagaa ccaacaacac ccttcccagc ctttcctttc cctcgccctc 2655
ttctcgtccc ctaagcaaac aacatccgct tgcttctgtc tgtgtaacca cagtgaatgg 2715
gtgtgcacgc ttggtgggcc tctgagcccc tgttgcacaa accagaaaca gagcagagcc 2775
aaggggggcct gacaagagtt ccttttagc tgaacaaaca agtgctctcc ataataggtg 2835
gaatcagaca gttaacacat ttttatgttg aaaacaaaat aaaaggaaaa aattaaaaaa 2895
aactatcatg aactgtattg ctccagttcc catccccaag tggcccagcc ctttcttgct 2955
ggtccagctg gacaggagca gcnatctaga atcaggatgc ggggagtgag gaagtttttc 3015
ctttgacaat gaaggtgggc tttcattgtg atttttgttc tgttgcagta atataggagc 3075
acattttggc cattgtaatt acagggaaca aagggattgc ggacacatat ctggacttct 3135
tttcctccct tattgttgtg gaagagacac tagaaatgct caaacacctg caatatacag 3195
aatatacaca attttattcc agtatttccc taacatatgg tttaaaatta ttccaggtat 3255
acagtgtatg caattctgca ttatcacaga ggaacaactt ctttttaaa aaataaatag 3315
gtcagccatt tttattaacg tgcaaaaact ttatcactct aacatgctct aggtagttga 3375
ggaaaagagg tctgatcact gtttgtattt tattttcttt gtgggaacat ttcacctgct 3435
gagtgtacat gaatttgctt tctataaaag gcttttatga gtttacagta gaatcagtgg 3495
aaggaagagt taataagggc tgtttttaaa aaaacaaaca aacaaacaaa acaaataatt 3555
aaaaaaaaat tttacattcc ttcctattct ctaactacac ttgggaagtg cacttcagat 3615
aagtttgcag tgtgactgag agatgaagga aatccataga aaaggtcctc ttagtgaaca 3675
aaatttagtt attaacttta tagctatgaa atttccccgg gcatttgttt ttgttcaaac 3735
agactttaac ctctgcatca tacttaaccc tgcgacatgc gtacagtatg catattttgt 3795
tttgaaaaaa aatgtttcgt tccagtctgt taagaatatt caaaaataat aaaggtattg 3855
cttaataaaa ttgctagaat tgtttagcag tacatgcaca atattttact agattctttg 3915
ttttaatagt gttttgttga gactgaaaat cttaaaatgg tctgcgcaaa tacaaaaaaa 3975
agaaaacacc aaaaatgcaa aattctcccg tttttgttcc tttttaaaaa tttttttttc 4035
tgcaaatgca aatacattca catgtggaca gatacataca cataggcatc atattttagt 4095
gtatggaaac atggtgcttt tctggggaca caagctgagg aagtgaatgg ctcgggggag 4155
acacattaat tgcatggaat tgttgactgt gaaacacttg tagaaatgag cactttggta 4215
tcccaaccaa tggtggaata cagatttcaa tggcgctggg gggacgagaa gcagaggaat 4275
tgaggctgca agtgattcct gaggaagagc tcacagggtg attttattca gatgacctct 4335
aagggaatgg ctaggaagga gtctgttctg acctttatct acctctgctg tggtaaggcc 4395
actccatgtg ccatctcacc atctcttcag cgttcctcat gctgcttctc cccgtgccat 4455
aggcgtttcc attcttgcag gaaaatgaya atgcaagtgc aaattccact cacttttatt 4515
ggtatgacaa taaattattc tttctaaaca cttagcaaaa tgacgaaaag cagtattcct 4575
taaaatatag gttttcattt tctcaatata ttttgaactg actaaagttc tttacaaaga 4635
caagaggatc agaaggttcc acttacccgt gttttagcgt ttgtttgaag ataatgncaa 4695
ncaaaaggtg gaaaactaaa accaccattg ctttacataa gaggtacaca ctgcccccca 4755
cccccaaaaa aaaacacagc tttgaaagtt gggagaaaca ctgcagtctt cattgtaaat 4815
ataaagtgat aatttaggtg aggaaggaac ggtaaggagg gaaggggaat gagtcctttc 4875
tccccatcaa gtcagccagc attggaatag tctctaattc tggcggaata ttttctttgt 4935
catgttcatc tattcttatt acaggagaat gatttcagtg cctagtattt attagtgtaa 4995
gtgtgtaacc actttcccgc aatatttcca ctggacatgt tgaagcaaag cagcttcttc 5055
tggggtcagg cagaggatcc aaataggcaa cgactccttt cccaagctca gaaacaatca 5115
ctgatgatgc agatttcact acatccgttg attctttgta gtagttttcc tggcacacac 5175
ttgagcatgc ttaaggttgt gcatatgttc attttgaaca aataagttca gcccctgctc 5235
ctttgtaatc atcatcttgt ttagtttttc ctgtagagga tgtctaccgt atactggcta 5295
atgaactaca atattaaaat aattatttct gcaagcaagt tgaaaaccaa gaaaacaata 5355
tttgtttcat aaatgtatgg catagatttc cctgtttatt attcttttta tctgcaatag 5415
agaaatttca gtttctggaa tatgttggta ctgctaagct aaatggcaaa naacatagag 5475
ttcaatgtca ttctttattg catttacatt tggtgatacg ttatattgaa cttttcttgc 5535
attaaaaaga tagtattttt cccctctctc a 5566

<210> 5

<211> 458
<212> PRT
<213> Homo sapiens

<400> 5
Met Thr Arg Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys
1 5 10 15
Ile Trp Leu Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser
20 25 30
Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
35 40 45
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
50 55 60
Thr Arg Ala Arg Asp Lys Glu His Gln Gln Gln Gln Arg Gln Gln Gln
65 70 75 80
Gln Gln Gln Gln Gln Gln Arg Gln Arg Gln Gln Gln Gln Gln Gln Arg
85 90 95
Arg Gln Gln Glu Pro Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu
100 105 110
Ser Ser Pro Ala Ala Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser
115 120 125
Pro Thr Leu Pro Pro Ser Pro Gly Asp Gly Gly Gly Gly Gly Gly Lys
130 135 140
Gly Asn Arg Gly Lys Asp Asp Arg Gly Lys Ala Leu Phe Leu Gly Asn
145 150 155 160
Ser Ala Lys Pro Val Trp Arg Leu Glu Thr Cys Tyr Pro Gln Gly Ala
165 170 175
Ser Ser Gly Gln Cys Phe Thr Val Glu Asn Ala Asp Ala Val Cys Ala
180 185 190
Arg Asn Trp Ser Arg Gly Ala Ala Gly Gly Asp Gly Gln Glu Val Arg
195 200 205
Ser Lys His Pro Thr Pro Leu Trp Asn Leu Ser Asp Phe Tyr Leu Ser
210 215 220
Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu Phe Ser Gly Leu Ser Ser
225 230 235 240
Pro Asn Thr Leu Asn Cys Ser Leu Asp Val Val Leu Lys Glu Gly Gly
245 250 255
Glu Met Thr Thr Cys Arg Gln Cys Val Glu Ala Tyr Gln Asp Tyr Asp
260 265 270
His His Ala Gln Glu Lys Tyr Glu Glu Phe Glu Ser Val Leu His Lys
275 280 285
Tyr Leu Gln Ser Glu Glu Tyr Ser Val Lys Ser Cys Pro Glu Asp Cys
290 295 300
Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser Gln Tyr Phe Glu Val Thr
305 310 315 320
Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys Lys Gln Tyr Cys Leu Glu
325 330 335
Val Gln Thr Arg Cys Pro Phe Ile Leu Pro Asp Asn Asp Glu Val Ile
340 345 350
Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr Gly Leu Tyr Glu Thr Phe
355 360 365
Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp Val Arg Arg Glu Glu Lys
370 375 380
Ser Asn Asn Pro Ser Lys Gly Thr Val Glu Lys Ser Gly Ser Cys His
385 390 395 400
Arg Thr Ser Leu Thr Val Ser Ser Ala Thr Arg Leu Cys Asn Ser Arg
405 410 415
Leu Lys Leu Cys Val Leu Val Leu Ile Leu Leu His Thr Val Leu Thr

```
            420                 425                 430
Ala Ser Ala Ala Gln Asn Thr Ala Gly Leu Ser Phe Gly Gly Ile Asn
        435                 440                 445
Thr Leu Glu Glu Asn Ser Thr Asn Glu Glu
    450                 455
```

<210> 6
<211> 1791
<212> DNA
<213> mus musculus

<400> 6

```
agccctcacg ggtggagtgg agtcggccag ggctgtgcgt tcccaaaat atg acc agg      58
                                                      Met Thr Arg
                                                      1
ggt gct tgg atg tgt cgg cag tat gac gac ggc tta aaa atc tgg ttg      106
Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys Ile Trp Leu
    5                   10                  15
gca gca ccc cgg gag aac gag aaa ccg ttc atc gat tca gag cgg gct      154
Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser Glu Arg Ala
20                  25                  30                  35
cag aaa tgg cga ctg tct ctg gct tct ctc ttg ttt ttc aca gtc ctg      202
Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe Thr Val Leu
                40                  45                  50
ctc tct gat cac ttg tgg ttc tgc gcc gag gcc aag ctg acc cgg acc      250
Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu Thr Arg Thr
            55                  60                  65
cgg gac aaa gag cat cac caa cag cag cag caa cag cag caa cag cag      298
Arg Asp Lys Glu His His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
        70                  75                  80
cag caa cag cag caa cag cag cag cag cag cag cag cga cag cag cag      346
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Arg Gln Gln Gln
    85                  90                  95
cgg cag cga cag cag cag agg cag cga cag cag gag ccc tcc tgg ccc      394
Arg Gln Arg Gln Gln Gln Arg Gln Arg Gln Gln Glu Pro Ser Trp Pro
100                 105                 110                 115
gcg ctc ctg gcc agc atg ggg gag tcc tcg ccc gcc gcc cag gca cac      442
Ala Leu Leu Ala Ser Met Gly Glu Ser Ser Pro Ala Ala Gln Ala His
                120                 125                 130
aga ctc ctc tcc gcc tcc tcg tcc ccc acc ctg ccc ccc tcc ccg gga      490
Arg Leu Leu Ser Ala Ser Ser Ser Pro Thr Leu Pro Pro Ser Pro Gly
            135                 140                 145
ggc ggc ggc ggc agc aag ggc aac cga ggc aag aac aac cgg agc agg      538
Gly Gly Gly Gly Ser Lys Gly Asn Arg Gly Lys Asn Asn Arg Ser Arg
        150                 155                 160
gct ctt ttt cta gga aac tct gcc aag ccg gtg tgg cgc cta gag act      586
Ala Leu Phe Leu Gly Asn Ser Ala Lys Pro Val Trp Arg Leu Glu Thr
    165                 170                 175
tgt tac ccc cag ggc gcc tcc tcc ggc cag tgc ttc acc gtg gag agc      634
Cys Tyr Pro Gln Gly Ala Ser Ser Gly Gln Cys Phe Thr Val Glu Ser
180                 185                 190                 195
gcg gac gct gtg tgc gcc agg aac tgg agt cgg ggg gcg gcc gcg ggg      682
Ala Asp Ala Val Cys Ala Arg Asn Trp Ser Arg Gly Ala Ala Ala Gly
                200                 205                 210
gag gag cag tcg tcc agg ggc tct cgg cca act ccg ctg tgg aac ttg      730
Glu Glu Gln Ser Ser Arg Gly Ser Arg Pro Thr Pro Leu Trp Asn Leu
            215                 220                 225
tcg gat ttt tac ctt tca ttt tgt aat tcc tac aca ctt tgg gag ttg      778
```

```
Ser Asp Phe Tyr Leu Ser Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu
        230                 235                 240
ttt tcg ggg ctg tcc agc ccc agt act ttg aac tgc agt ctg gac gtg      826
Phe Ser Gly Leu Ser Ser Pro Ser Thr Leu Asn Cys Ser Leu Asp Val
    245                 250                 255
gtg ctc acg gag ggc ggt gag atg acc acg tgt aga cag tgc atc gag      874
Val Leu Thr Glu Gly Gly Glu Met Thr Thr Cys Arg Gln Cys Ile Glu
260                 265                 270                 275
gct tac cag gac tac gac cac cac gct cag gag aag tac gaa gag ttt      922
Ala Tyr Gln Asp Tyr Asp His His Ala Gln Glu Lys Tyr Glu Glu Phe
                280                 285                 290
gaa agc gtg ctg cat aag tac tta cag tcg gat gag tac tcg gtg aag      970
Glu Ser Val Leu His Lys Tyr Leu Gln Ser Asp Glu Tyr Ser Val Lys
            295                 300                 305
tcc tgt cct gag gac tgc aag att gtc tac aaa gcc tgg ctc tgc tcc     1018
Ser Cys Pro Glu Asp Cys Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser
        310                 315                 320
cag tat ttt gaa gtc aca cag ttt aac tgc aga aag acc att cct tgc     1066
Gln Tyr Phe Glu Val Thr Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys
    325                 330                 335
aag caa tat tgc ttg gag gtg cag aca agg tgt cca ttc ata ttg ccc     1114
Lys Gln Tyr Cys Leu Glu Val Gln Thr Arg Cys Pro Phe Ile Leu Pro
340                 345                 350                 355
gac aat gac gaa gtc att tac gga ggc ctc tcc agc ttc atc tgc aca     1162
Asp Asn Asp Glu Val Ile Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr
                360                 365                 370
ggg ctc tac gaa acc ttc cta acc aat gat gaa ccc gaa tgc tgt gac     1210
Gly Leu Tyr Glu Thr Phe Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp
            375                 380                 385
atc agg agc gag gag caa acc gca ccc aga ccc aaa gga acc gtg gac     1258
Ile Arg Ser Glu Glu Gln Thr Ala Pro Arg Pro Lys Gly Thr Val Asp
        390                 395                 400
aga aga gac tcc tgt ccc agg aca tcg ctc aca gtg tcc tcg gcc act     1306
Arg Arg Asp Ser Cys Pro Arg Thr Ser Leu Thr Val Ser Ser Ala Thr
    405                 410                 415
aga ctg tgc ccc ggc cgg ctg aag ctg tgt gta ctc gtc ctc att ctc     1354
Arg Leu Cys Pro Gly Arg Leu Lys Leu Cys Val Leu Val Leu Ile Leu
420                 425                 430                 435
ctc cac aca gtg ctc acg gcc tcc gca gcg cag aac tcc acg gga ctg     1402
Leu His Thr Val Leu Thr Ala Ser Ala Ala Gln Asn Ser Thr Gly Leu
                440                 445                 450
ggc ctg ggt ggc ctc ccc acg ctc gag gac aac tcc acc cgg gag gac     1450
Gly Leu Gly Gly Leu Pro Thr Leu Glu Asp Asn Ser Thr Arg Glu Asp
            455                 460                 465
tga gcgcagccag gcgcgtgcgc agagcgcagg gctgggcagg gacacgcgct          1503
 *
tggcacagag cagcagtgac ccaccgggga tgctcacctg ctgcagcccg ggaactgaac  1563
ccacccgggt gctctaccct tggacttctc gcaaggcctg tgggtaacat tcaacaagat  1623
gggcccgatc cccaacatgg acacagccgc agctttttgc cgactaaaag gctgcaagtg  1683
actcagtttc tcacaccatt ttatacactg tgttttaacg tttggaggtt ttctttgctt  1743
tcagttcggt ttgggtttat tttccgtttt taaacttttt tttttttg               1791

<210> 7
<211> 467
<212> PRT
<213> mus musculus

<400> 7
```

```
Met Thr Arg Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys
1               5                  10                  15
Ile Trp Leu Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser
            20                  25                  30
Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
        35                  40                  45
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
    50                  55                  60
Thr Arg Thr Arg Asp Lys Glu His His Gln Gln Gln Gln Gln Gln Gln
65                  70                  75                  80
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Arg Gln
                85                  90                  95
Gln Gln Gln Arg Gln Arg Gln Gln Gln Arg Gln Arg Gln Gln Glu Pro
            100                 105                 110
Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu Ser Ser Pro Ala Ala
        115                 120                 125
Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser Pro Thr Leu Pro Pro
    130                 135                 140
Ser Pro Gly Gly Gly Gly Gly Ser Lys Gly Asn Arg Gly Lys Asn Asn
145                 150                 155                 160
Arg Ser Arg Ala Leu Phe Leu Gly Asn Ser Ala Lys Pro Val Trp Arg
                165                 170                 175
Leu Glu Thr Cys Tyr Pro Gln Gly Ala Ser Ser Gly Gln Cys Phe Thr
            180                 185                 190
Val Glu Ser Ala Asp Ala Val Cys Ala Arg Asn Trp Ser Arg Gly Ala
        195                 200                 205
Ala Ala Gly Glu Glu Gln Ser Ser Arg Gly Ser Arg Pro Thr Pro Leu
    210                 215                 220
Trp Asn Leu Ser Asp Phe Tyr Leu Ser Phe Cys Asn Ser Tyr Thr Leu
225                 230                 235                 240
Trp Glu Leu Phe Ser Gly Leu Ser Ser Pro Ser Thr Leu Asn Cys Ser
                245                 250                 255
Leu Asp Val Val Leu Thr Glu Gly Gly Glu Met Thr Thr Cys Arg Gln
            260                 265                 270
Cys Ile Glu Ala Tyr Gln Asp Tyr Asp His His Ala Gln Glu Lys Tyr
        275                 280                 285
Glu Glu Phe Glu Ser Val Leu His Lys Tyr Leu Gln Ser Asp Glu Tyr
    290                 295                 300
Ser Val Lys Ser Cys Pro Glu Asp Cys Lys Ile Val Tyr Lys Ala Trp
305                 310                 315                 320
Leu Cys Ser Gln Tyr Phe Glu Val Thr Gln Phe Asn Cys Arg Lys Thr
                325                 330                 335
Ile Pro Cys Lys Gln Tyr Cys Leu Glu Val Gln Thr Arg Cys Pro Phe
            340                 345                 350
Ile Leu Pro Asp Asn Asp Glu Val Ile Tyr Gly Gly Leu Ser Ser Phe
        355                 360                 365
Ile Cys Thr Gly Leu Tyr Glu Thr Phe Leu Thr Asn Asp Glu Pro Glu
    370                 375                 380
Cys Cys Asp Ile Arg Ser Glu Glu Gln Thr Ala Pro Arg Pro Lys Gly
385                 390                 395                 400
Thr Val Asp Arg Arg Asp Ser Cys Pro Arg Thr Ser Leu Thr Val Ser
                405                 410                 415
Ser Ala Thr Arg Leu Cys Pro Gly Arg Leu Lys Leu Cys Val Leu Val
            420                 425                 430
Leu Ile Leu Leu His Thr Val Leu Thr Ala Ser Ala Ala Gln Asn Ser
        435                 440                 445
Thr Gly Leu Gly Leu Gly Gly Leu Pro Thr Leu Glu Asp Asn Ser Thr
    450                 455                 460
```

Arg Glu Asp
465

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713LF1

<400> 8
cgcttgcttc tgtctgtgta acc 23

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713LR1

<400> 9
gtatttgcgc agaccatttt aagatt 26

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 713.LF1.5.1

<400> 10
actgtctgat tccacctatt atggag 26

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713.LF1.5.1n

<400> 11
tgattccacc tattatggag agcac 25

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE5R1

<400> 12
gggtagaagg gagacttagg 20

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE5R-49

<400> 13
gggcatagca atcattc 17

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713CTGLF132

<400> 14
ggctgtgcgt tcccaaaata 20

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE3N

<400> 15
aaaaatgttt cgttccagtc tgttaaga 28

<210> 16
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE3Nn

<400> 16
attgctagaa ttgtttagca gtacatgca 29

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1polyA

<400> 17
ttttttttttt tttgacagag 20

<210> 18
<211> 25
<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LR100

<400> 18
tttgccattt agcttagcag tacca 25

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713.PU

<400> 19
aatattctta acagactgga ac 22

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713.RP

<400> 20
ctttatagct atgaaatttc cc 22

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g34301.PU

<400> 21
ctgatcactt gtggttctgc gccg 24

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g34301.RP

<400> 22
aggactcccc catgctcgcc ag 22

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide SG1LR1102

<400> 23
aaaatactgg gaacagagcc agg 23

<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LF790

<400> 24
gcacttagag cgcggggt 18

<210> 25
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LF834

<400> 25
gccggaggca gccca 15

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTGR1511

<400> 26
tgtcctcgag cgtgggg 17

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTGLR20

<400> 27
cggaggaggg gatacggaaa ttaaacc 27

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTG1440

<400> 28

tgggtcactg ctgctctgtg ccaag 25

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTG5RACE1

<400> 29
tcacagtgtc ctcggccact 20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTG5RACEn

<400> 30
tcctccacac agtgctcacg 20

<210> 31
<211> 983
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 14
<223> n=a, g, c or t

<400> 31
aaaaaaaaaa aaanaacaaa aacaaaacat gaaacaggaa gacaggaaag atccatttga 60
cagagtactt gacacaggag agagaagaaa tactcatgta tctgaaagta ttcaaagggg 120
gagtgttagg agatgaatta atttaaaaaa tgagtaagag taaaatagtt taaagttaga 180
ccctgaggaa ctccagggaa gacaaagtaa cacaaggaac aagcaatgtt agccactgcc 240
taactttcct cagggtcatg tgtgcctcgc cataattatg taaacactta cattgttaaa 300
acgaaattcg gagaactagt ttgagtaaag gggaaaagaa agtatgttat tcatgtcgga 360
gttggaaata tgtgataggt tgaaattctc aatttcctaa ttggaaatca ttaagtcata 420
ctgaaacctg aaaattcaag aactgacaac acaattgatg ttgagatatg gaatttggta 480
cctgatgaaa gattagaaaa ttattaaaag caatttcttc tgggtggtgc tacaagatgg 540
aagaagaaag gacagaaagc tcttcataat caggtagacg ctttgacttt ttaagtggta 600
tgcctatatg cctttaaaaa acaactcaat ttaaaagaaa attaagagat gctaacagcc 660
gatttaaaga aaatttagta aaatattcaa ttgtataaag atacacaaaa tattggttat 720
ctacatgata gcaaagatga attaagggat ggggataaaa ctcttctcaa taacaccaaa 780
attaaaataa aacataattc atatatttag aaatatcatt acagaaatat gttgaacttg 840
tattaacagc ctctcctcaa aggtagcatg gagaatcatg caaacttaat ttggagatac 900
aaaaaaaatt gagaatgtgt agtgttgttc tttaattcta actgtaatgg ctgaataata 960
ttttgatcat gattgtgata cta 983

<210> 32
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 298
<223> 99-15663-298 : polymorphic base C or T

<220>
<221> misc_binding
<222> 275..321
<223> 99-15663-298.probe

<220>
<221> primer_bind
<222> 279..297
<223> 99-15663-298.mis

<220>
<221> primer_bind
<222> 299..317
<223> 99-15663-298.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15663.pu

<220>
<221> primer_bind
<222> 430..450
<223> 99-15663.rp complement

<400> 32
tcccaccttc ttctaaacgt gttgcttcaa tacgttgata ggtgaggaca cttaaaaatt 60
agactttata gaaataggtt ttttttttgtt tacatatata gttcttttgg tatcatatat 120
ttagcctctt tctaaaattt atttttttgat actgaaggga gaaataggga gttattaatc 180
aacaggcatt aattttagtc aagcaaaata aataagctgt agcgatctgc tctgtaacat 240
tgtacctaca gccaacaatt atatgttgtc cacttaaaaa tgtgttagat ctcatagyaa 300
ctcttcttac cacaataaag taaaaattct gaaacaataa gtgaatacct aaataataca 360
aacaaataca atattgtagt tttgggcact taataaatga cagcctcatt tctcaattag 420
agatcatcac aagttagaca gatgacgatg 450

<210> 33
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 398
<223> 99-15665-398 : polymorphic base A or G

<220>
<221> misc_binding
<222> 375..421
<223> 99-15665-398.probe

<220>
<221> primer_bind
<222> 379..397

<223> 99-15665-398.mis

<220>
<221> primer_bind
<222> 399..417
<223> 99-15665-398.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-15665.pu

<220>
<221> primer_bind
<222> 458..476
<223> 99-15665.rp complement

<400> 33
cgtaaatgtg aaaagcatag cctcttcttg gaatgttaag tataaatatc tgaaatactg 60
ggcttgatat gtcaacagga gattgatgga taaaaataga attttatata aaaaacaact 120
ggacatatta gattgttaac ttggaagaaa gaccatattc aaagaagaaa acatagtgac 180
taatttcaaa catttaaagt cttccctgtg gaaacaaagg aatatctttg ttctaacact 240
tcaaagaaca gggttaaaaa atagactcac cacagagtaa atgcacaatt gacaatcgtg 300
aatgaattaa aaaccaaaca aaatattttg tcagctttct atctatgaaa ctaagaaaca 360
ggcttcctac taaggtaatg aatgtaattc acagagarca ttcacgtata agtttcattc 420
atgtttcaaa tttcattgat ttgatcaatg ggttattcta ataccctccc ttattt 476

<210> 34
<211> 547
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 166
<223> 99-15672-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 143..189
<223> 99-15672-166.probe

<220>
<221> primer_bind
<222> 147..165
<223> 99-15672-166.mis

<220>
<221> primer_bind
<222> 167..185
<223> 99-15672-166.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15672.pu

<220>

<221> primer_bind
<222> 533..551
<223> 99-15672.rp complement

<400> 34
ccaataccat aactcctcta taggacatgg aagagtatta tatatgacaa atgattgcta 60
tgattattat tatcagtgtt attattatcc taatcctaag taatccaata aaagaaaaat 120
acatctgtgc ctgtgcgtat gtgcacgtgt gtgcagtcaa atacaygttg agtaaaggta 180
aagtctagct gtatttaatc aacctacctg aatcctcagg aaaaaattct aaacctagtt 240
taaaacatgt aaactctaag ctctctcctt atagtcagtt agtagcagca catcttaaaa 300
tctggtgtga atattctctt agttctacat gagtctaact aaacagagga ttattcttag 360
gtgtttgaaa gagacatatg tgacactgct gttttgagaa caatttaagt gttgtcttgt 420
catgtacaga agttctcata ttactttaca taaatggttg cataattgtt ttatagtaaa 480
taatagactg tcaatatttc taggataact ccaaaacaaa atttcctaga mmacattttg 540
aaaaggg 547

<210> 35
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 185
<223> 99-15664-185 : polymorphic base G or T

<220>
<221> misc_binding
<222> 162..208
<223> 99-15664-185.probe

<220>
<221> primer_bind
<222> 166..184
<223> 99-15664-185.mis

<220>
<221> primer_bind
<222> 186..204
<223> 99-15664-185.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15664.pu

<220>
<221> primer_bind
<222> 483..502
<223> 99-15664.rp complement

<220>
<221> misc_feature
<222> 54
<223> n=a, g, c or t

<400> 35
gtttaccatt agcactgtca tatttgtgtg acttgtcatt ctctacagcg gagnacgggc 60

tggcacgggg cctgatgctg acttgcacaa gggaagcctc ctgtctctga cttccccagg 120
ataattcctg gggaaagtgt gctccctagt gttaagagcg gtttaatggc tggagggttt 180
cagckggctg accaggcaga gaaggagggt gaatcacctc tcagcactct ccacttagac 240
tttgtgtggt cgtcgggtgg tcaaaccttc taactagttg tattgcagat ttggcattcc 300
agtgcaaaca aaagacagaa acacaatgtt cacatgcttt ccagagatca cctggatatc 360
agatcatttg attttcaagt aagtcgaaac cttggtggaa atcattaact atcctgttta 420
tgaccaaaaa ataaaatccc aaatttcttc tcttcatttc ttacctgctt taaaattgta 480
tccaaagcgt graagtaaaa ga 502

<210> 36
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 205
<223> 99-5919-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 182..228
<223> 99-5919-215.probe

<220>
<221> primer_bind
<222> 186..204
<223> 99-5919-215.mis

<220>
<221> primer_bind
<222> 206..224
<223> 99-5919-215.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-5919.pu

<220>
<221> primer_bind
<222> 435..455
<223> 99-5919.rp complement

<400> 36
ctacagcaat gcagatttca attctgccat tgaattccca gacatattcg tcatccccat 60
tttcatcccc caccaccctg ccattttctt cgtgttaact tgttttcctg actcacagaa 120
atcacctttt cctgtataca tttttaggat gtcagacttt attctaatga tttctcctag 180
ttgccccccа aaattgtatt ctacrgtgtg attttaaagc tgaattttca agatgatatt 240
tcatatctat attttcacaa gcttttcttc tatgaatgtt attgtcagct gtcagggtgt 300
gagatggtac ttgatactac attctttcca agctgttgcc tgaatcggtt taagacaaag 360
tcattactag gctgtaaact gttgctctgc aaaattgagc agcacgtatt taaccactca 420
tacttcttag ctctccaaca ctttgagtca ataga 455

<210> 37
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 157
<223> 99-5862-167 : polymorphic base C or T

<220>
<221> misc_binding
<222> 134..180
<223> 99-5862-167.probe

<220>
<221> primer_bind
<222> 138..156
<223> 99-5862-167.mis

<220>
<221> primer_bind
<222> 158..176
<223> 99-5862-167.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-5862.pu

<220>
<221> primer_bind
<222> 430..450
<223> 99-5862.rp complement

<400> 37
aatcaaggta gagatgtatg agaaatagcc ggttaaagaa acagcattac tttcagacta 60
tcttttattt gaaatacacg tggggaaacc agaaggtgaa acccccttagg agatggatat 120
aggatactaa aatctgagtt agaaaaattt gagcatyagc accttacgtg tcatgctaag 180
atagtgaatg agactgcaca ggaattgcat gcagtttaac ggaaaaagaa gtcgaaagat 240
aaattcctag aacactaaca ccgagttatg ggaggagaaa tatcctgcac aggtcactct 300
gggagacatg tcaattgttt agccaatatc catttaactc atctttcttc ctaatgaaaa 360
ccgaatttgg agaagcaggt agtgcccctg gctagaaata tgaaccttcc cagcttctct 420
catgcactga actgacaaag ttcaggtctg 450

<210> 38
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 292
<223> 99-16032-292 : polymorphic base A or C

<220>
<221> misc_binding
<222> 269..315
<223> 99-16032-292.probe

<220>
<221> primer_bind

<222> 273..291
<223> 99-16032-292.mis

<220>
<221> primer_bind
<222> 293..311
<223> 99-16032-292.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16032.pu

<220>
<221> primer_bind
<222> 384..403
<223> 99-16032.rp complement

<400> 38
gttgttaccc cacttcttcc ccccagctcc cccttcctca cacagttcat gccacatgcc 60
actctcctgg actactggaa atgcgtcagt ccactctggg ctcatcccat catcccccat 120
gctgcaacct gagagagagt tgcaagttgc aaatctgatc ttgtcaccac cactctccac 180
actaaatccc tctaatgcct ccccctttct ttttggataa attccttctg cttgcatagc 240
cacgtggttg gcttctatag catcacttca cactgtggtc acctgccttc tmctcactca 300
ggaacttctc tccattgaag aagttcttct tccccatctc cagggctttc ccactgacag 360
ttgtatctcc cccataccaa gcccaggtgg tcatctcatc cca 403

<210> 39
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 118
<223> 99-16038-118 : polymorphic base A or G

<220>
<221> misc_binding
<222> 95..141
<223> 99-16038-118.probe

<220>
<221> primer_bind
<222> 99..117
<223> 99-16038-118.mis

<220>
<221> primer_bind
<222> 119..137
<223> 99-16038-118.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16038.pu

<220>

<221> primer_bind
<222> 456..476
<223> 99-16038.rp complement

<400> 39
gttgcttatt ctttctctct tctgcagggt ataaaggaat ctgaacacga ctgatatttt 60
ctttaatttt tagatccaga tatacattgg gtaaaatcta cttcataggt tttcaaarga 120
gcattcttct gagcaaatct gaaaactctc taaactctat tggtatgtta ctctttatct 180
ttatatgaat ttaaattctt ctagaagtta gataaaactg tggtaaagct acataatact 240
tttgacatat tttcaagcgt agacaaactt caattaattt gtaagataca ggaagaaaat 300
ttttccagtt aaaatgtacc tcttggtttc tggagtgtta gcaaccattc acacttacag 360
ttcaaacagt gcaaccttgt aaaacatata taacttatga agagatcgat atctcttttt 420
ataaagcaaa caagtaaatt tttccctcaa tccatgattt atttttgtga agtggg 476

<210> 40
<211> 498
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 133
<223> 99-5897-143 : polymorphic base A or C

<220>
<221> misc_binding
<222> 110..156
<223> 99-5897-143.probe

<220>
<221> primer_bind
<222> 114..132
<223> 99-5897-143.mis

<220>
<221> primer_bind
<222> 134..152
<223> 99-5897-143.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-5897.pu

<220>
<221> primer_bind
<222> 475..492
<223> 99-5897.rp complement

<400> 40
aaaagtgttt gccagtcctg tttcttacag agcacagaac tcagatgctc ttataaagat 60
acaggataaa tcacatcatt tcctgctcca tcatcagaat attattatat gatttagatc 120
actttttaa aamagaacat ggacttagta cagaacaaca gcaaaagcct ggggaaggag 180
aggagtgcac catgaggagt caatggggag cagaagccag tccatttgac tgatttggtt 240
cgtgtgcaaa ataattgcta aataattgca tatatgtgag actccgggta ttttcaaaac 300
cagctggcaa aattgtgtta ttctctaccc tctgctggct ttcacgggtt ctctgttctc 360
tctccttttc ctccattctc ctcttaccct aattcctgac cactgtaatc caataatcta 420
aggttttagg atttggatga ctaaggttac ccatggaatt gtttggaaat gtagacctgt 480

aatggagagg ggagaaaa 498

<210> 41
<211> 517
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 360
<223> 99-13601-360 : polymorphic base A or G

<220>
<221> misc_binding
<222> 337..383
<223> 99-13601-360.probe

<220>
<221> primer_bind
<222> 341..359
<223> 99-13601-360.mis

<220>
<221> primer_bind
<222> 361..379
<223> 99-13601-360.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-13601.pu

<220>
<221> primer_bind
<222> 500..517
<223> 99-13601.rp complement

<400> 41
gttttacttg acagttacca agaattgttt cgcatttaag aaaattatat ctttgatggt 60
tccctcatta atggtgcctg gatacccaat gcaacacacc tacatcaaac tgcatttgta 120
actgttggat tcataatgat tctacctaag atgcaagcat acggcatcat tgtgccttgt 180
tgtatggata tgcttgagaa gtcacatgct gaaatacata tattttaaat ttgacagtat 240
ctcctacaat attttcttta tattatagta aggtattaca ttacagttta aaacttatga 300
ctataagcag gtgatattat ctatgaattt catgtgaaat tagcaaaggg acagtctcar 360
atgtttgctg tataaagtgt atttgaagcc tgatagggtt gagaaacact cagctacagt 420
aagtaaaaac agctctctta gtggttgcct tgttgagaag atcttgaaaa caaggttgaa 480
aatacaaaag aaactgtgtg gagtctacaa agatatt 517

<210> 42
<211> 533
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 97
<223> 99-13925-97 : polymorphic base A or G

<220>
<221> misc_binding
<222> 74..120
<223> 99-13925-97.probe

<220>
<221> primer_bind
<222> 78..96
<223> 99-13925-97.mis

<220>
<221> primer_bind
<222> 98..116
<223> 99-13925-97.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13925.pu

<220>
<221> primer_bind
<222> 513..533
<223> 99-13925.rp complement

<400> 42
catggaagta aaagcatatc ttcattataa gacttctaca caaattatca catctttact 60
tacagcagct gaaacctgga aacaactcta atgcccrtca acagaggaat ggatggataa 120
agaaactgtg atgcagtgga atacgactca acgaagatga gactaaaaat aattatactg 180
agtaaaagaa tccaaacaaa atagagcaaa cactgtgcca tcctgtttat accttactcc 240
agtaaatgca aactaataca caatgaaaaa aattacttat ttgagaactg gggagaggaa 300
ggagagggaa aggggtagat aaagaaaaga ggagagatta aaaggagcat aagaaaacct 360
cagagaataa taggtttgtg gtaaacatta ccgtggtaat gtttttaggg tatattcaca 420
tgtaaaaact tatccaatta tacattttaa atatgtacag tttagtgtgt cagttatgcc 480
tctgtaaagt tgattttaaa aaaagtccta ttccaagtym acaatttcat ttg 533

<210> 43
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 201
<223> 99-13929-201 : polymorphic base A or C

<220>
<221> misc_binding
<222> 178..224
<223> 99-13929-201.probe

<220>
<221> primer_bind
<222> 182..200
<223> 99-13929-201.mis

<220>
<221> primer_bind

<222> 202..220
<223> 99-13929-201.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-13929.pu

<220>
<221> primer_bind
<222> 460..480
<223> 99-13929.rp complement

<400> 43
gggagaatac taataatgga agcattactt ttatttttc tataaattcc tctggaaata 60
tgtatttctt atgtcctaag gttattaaca aaaagagaaa ataatttctg atttataatt 120
cactttcctt caaaaaataa taactcagtg tctagtaagg taaagcaaaa aaagttaaaa 180
gaacccataa gtttatttta maatacctac tcagaagcaa aactgacttt ctattaaaaa 240
ttaaaaaaaa aagttttctt attattgttt tgtttccttg tttttaggtg atgggattgt 300
atttgcaact ctctggtcag taagtgataa aatgccattt ctatgcaccc acctggcctg 360
tgtgactggg agaatctctc tttttattaa atgtgcttca agttttaaca actgactttt 420
gttagtgata tgatttatct acccgtgact gtcaaacaac acagatgatt tgcatatctc 480

<210> 44
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 108
<223> 99-14021-108 : polymorphic base A or G

<220>
<221> misc_binding
<222> 85..131
<223> 99-14021-108.probe

<220>
<221> primer_bind
<222> 89..107
<223> 99-14021-108.mis

<220>
<221> primer_bind
<222> 109..127
<223> 99-14021-108.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-14021.pu

<220>
<221> primer_bind
<222> 460..477
<223> 99-14021.rp complement

<400> 44
tttgttgtta atcgcccctt ttctgcaaca cttgtgggtt agggaaaata attctaaagc 60
aagagcaaag acagagttgg gagatcacca gtgaggttca attttccrtc acattcactc 120
tgctccacac ctcagataat catgtgctta actgcgaaac ttgcttgaca attacagaac 180
actttctcac ccattactac cttgatcctc acaattctgt ggggtagtag gagcagatgc 240
tgaaattgcc atacgcaaat cagtgaactg aagcttagag acctccagca ggggcagagg 300
gtcagcggaa actatcccag ggttcagcca acaagaaagt atattggaat cagagtatta 360
aaataagaat aataaaacca actaaaattt accgtgcttt ttatttccac tcagtgccaa 420
caattcttaa cagtgtcagt gatggatccc tgtgccccag gggacagact tcttact 477

<210> 45
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 314
<223> 99-14359-314 : polymorphic base G or C

<220>
<221> misc_binding
<222> 291..337
<223> 99-14359-314.probe

<220>
<221> primer_bind
<222> 295..313
<223> 99-14359-314.mis

<220>
<221> primer_bind
<222> 315..333
<223> 99-14359-314.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-14359.pu

<220>
<221> primer_bind
<222> 457..475
<223> 99-14359.rp complement

<400> 45
ataagggaat ggtgtgaggt gggaccagag gaggctgcac tgagaaagtg agaggggcaa 60
gacctcaggg gaagaaggga gggctgcacg gatgtctcag gcagagcagg cagcaccgga 120
aaaggtgggg gacactcctt ttggaccagc atataatttg gttaaagcct ctcctgtttc 180
acctaatata taagcacatt tcaagataaa actactactt tattgtcatc aaatataaaa 240
gtaatttttt attcagggtt ttctaatact catctataaa ggcatttctt tcccacatgg 300
catgtgttac aggstgttta acttaaagca attgtaaaag aaaagcctga agaaataagt 360
ctacaacgat ttacatcgtg tttatttttg tgtcaaaata tatgttaaaa tatacattag 420
ctatactaag ggaatcaaga gaagatcata attgctctta tgacttggga tttag 475

<210> 46
<211> 473
<212> DNA

<213> Homo sapiens

<220>
<221> allele
<222> 316
<223> 99-14364-415 : polymorphic base C or T

<220>
<221> misc_binding
<222> 293..339
<223> 99-14364-415.probe

<220>
<221> primer_bind
<222> 297..315
<223> 99-14364-415.mis

<220>
<221> primer_bind
<222> 317..335
<223> 99-14364-415.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-14364.pu

<220>
<221> primer_bind
<222> 453..473
<223> 99-14364.rp complement

<400> 46
gtgttttaat tcaacccagc tataagatac gaaatgatag aattgctcta gattctctat 60
tggttaaata aggagatatt tgtgctattg ccaataatac atgctgtacc tggataaacc 120
cctttgggca agttgtgatg caaatactca agaaaatagg ccacatagtt acaacaggac 180
ttacctaatt ccccatggtc atttggctga ttcagtcagt tgctttcaag cctaggttct 240
tggctcaata ttattacata aactagaatt ttcctattac tattaatttt actttgtatt 300
tttctttata aacttygtac ttattgcttg tcaaatttca gcagaagtac aactcctgag 360
agaataatgc tggctcagag ttttgagatg ataacccttg tctatgaaac tgatgaagtt 420
ggacttaaca acgaacactc cccacagaac tcctgatgct caaatgtggc taa 473

<210> 47
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 99
<223> 99-15056-99 : polymorphic base C or T

<220>
<221> misc_binding
<222> 76..122
<223> 99-15056-99.probe

<220>

<221> primer_bind
<222> 80..98
<223> 99-15056-99.mis

<220>
<221> primer_bind
<222> 100..118
<223> 99-15056-99.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15056.pu

<220>
<221> primer_bind
<222> 482..502
<223> 99-15056.rp complement

<400> 47
caggaaactc acaagaagsc agatttcctt cgagcacctc ctgaataaag aggcaaaggc 60
cttcttaact cttacaattt acaagtggct atgagtgcyt ttatagttcc cataataatt 120
tctccacgta gacttcctaa ataataattt ctcctgtttt atattctctg tgcttatgtt 180
tatatcaaac aagttaccac ttaatcaaat gccgatttgc attgctcact atgtaacttt 240
aattttcttt gcctcttatt tttggatctt aattctaaaa ctagatgatc ataaattcat 300
ttaggaataa gcttgtgatc tagccttctt ttgaacccct ttgtgctcct cacaatattt 360
gtttcgatga aacagtgagc aacatttgat ctatgattgt taatagaaaa acaccaatgt 420
ctcaagttat tgtaaacata ggcataattg acctttggtt ctataaatat gtttggtgtt 480
ccccaaaata cgtctccctt tt 502

<210> 48
<211> 494
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 412
<223> 99-15229-412 : polymorphic base A or G

<220>
<221> misc_binding
<222> 389..435
<223> 99-15229-412.probe

<220>
<221> primer_bind
<222> 393..411
<223> 99-15229-412.mis

<220>
<221> primer_bind
<222> 413..431
<223> 99-15229-412.mis complement

<220>
<221> primer_bind
<222> 1..20

<223> 99-15229.pu

<220>
<221> primer_bind
<222> 476..494
<223> 99-15229.rp complement

<400> 48
ctgtcattga gaaatgctac caataatact tagagaattt gatacaactc agtctgaaaa 60
agctaagatt agcagaacag agctgtctcc aaatatttga agaactattt tatttaaggg 120
attggaccca tttttgtatg tagttccaga ggagcagatg gtgaccactg tccaggcaga 180
tgtgtctcaa tgtaaggaca acatctgtaa tattaataat tagaatgtat cctgtaattt 240
tctctctacc cttggaaacc agtcgagatc cagagtcttt cactgggagg cttaaagcct 300
agagcagcct tggtgctaga ggcggacagg gataatgaac taatcttgaa ccaattcatc 360
catagcaatc tcaatgcttt cgttagctct tataggtatt taatacggcc avaggaatga 420
aggtagtctt gctggtttag aagccctgcc taccacaacc cctacaccac cccatcccct 480
gcatagtctg atgt 494

<210> 49
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 291
<223> 99-15232-291 : polymorphic base G or T

<220>
<221> misc_binding
<222> 268..314
<223> 99-15232-291.probe

<220>
<221> primer_bind
<222> 272..290
<223> 99-15232-291.mis

<220>
<221> primer_bind
<222> 292..310
<223> 99-15232-291.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15232.pu

<220>
<221> primer_bind
<222> 467..485
<223> 99-15232.rp complement

<400> 49
caatagaaca ggctgctcct ttataattat taatcatagt gtatattaat tcatcatcac 60
atacgtggct agaaaaaaat ttagaacaaa aagatatgtg atatgtaaag gcctacgata 120
attcagactt ctttgaggag agcttttatt ttattgttat tcttatttta tctcttgtca 180
atataaattg agagaataaa cagacaaaca ttacaaatta gtgattaatt gcatttaaag 240

cctagttaag actatttaag actattatgc ataatacagg aaaactacct ktattattta 300
tagtgggtgc cttctgaagg atctgaagga gaatcagttc tatgcctctc tcctcattcc 360
caggaggtgc ctggcattcc ttggcttgta gacgcatcac cctaatctct acctctgcct 420
tcacatggtg tcccctgtgt gtgtgttttt gccccatgtg tctcctcttt ttatatggat 480
gccag 485

<210> 50
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 347
<223> 99-15241-347 : polymorphic base A or G

<220>
<221> misc_binding
<222> 324..370
<223> 99-15241-347.probe

<220>
<221> primer_bind
<222> 328..346
<223> 99-15241-347.mis

<220>
<221> primer_bind
<222> 348..366
<223> 99-15241-347.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15241.pu

<220>
<221> primer_bind
<222> 444..464
<223> 99-15241.rp complement

<400> 50
gttatgggtt gaaaatctct gagttcttgt acatacaaaa attttactgt tgtcacagtt 60
gaatcttagt ttagatgggt ataggatttt tattcaaaat gcttttactc cataagttta 120
aaaatattgt tacattttcc tcaagtatct gatgttattg atgagaagtt taattctaat 180
ttgactcttg ttcccttgta ggtactattt gttttccagt ttgggaagct tacatttctt 240
aaaattcaca acatataatt tacatactac acaattcttt ttaaagtata caattcaatg 300
catttagtat gttttagtac atataactta aattatgtat atacaaratc tctttataat 360
atttgtagaa tatgtagcat attcacaaga ttgttcaacc atcaccactc tctatttcca 420
gaatcttttc ctccaaaaag aaaccctgaa cactatgatg aata 464

<210> 51
<211> 550
<212> DNA
<213> Homo sapiens

<220>
<221> allele

<222> 196
<223> 99-15244-196 : polymorphic base A or G

<220>
<221> misc_binding
<222> 173..219
<223> 99-15244-196.probe

<220>
<221> primer_bind
<222> 177..195
<223> 99-15244-196.mis

<220>
<221> primer_bind
<222> 197..215
<223> 99-15244-196.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-15244.pu

<220>
<221> primer_bind
<222> 532..550
<223> 99-15244.rp complement

<400> 51
ctgcttctgg ttatgttttc ctaattgcca aaatggtaaa aatgagaata atcattgaaa 60
gagaaagcat aaagtagcaa aaatcctttc cagattaaaa aacgaagcaa agcatgtttc 120
ccaagtaata atactctcat cttcctccct aatcctttac cccactacca gaagaagagt 180
aaaatgtccg gatatrtttg aaggtaaaga tttctccttt taataaaatt agtcaccttg 240
tacacatcag tagatcttga gaatgaaaag cttttctagt acattcattt caacctataa 300
atgtttgact tttctctgtc attcatttac gacctgtgat cttttcattc cctttcagtt 360
agaatatttt tcaaattttt attgatattt tctatttaac ccataggtta tttggaaata 420
cattgtttaa tttctaatat atttgctttt ttttctactt atttcttttt ttcttaattc 480
cacactggtc caaatatatt ctgcatatga tttaatattt taagttctgt agagactaac 540
cttgtgccct 550

<210> 52
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 404
<223> 99-15252-404 : polymorphic base C or T

<220>
<221> misc_binding
<222> 381..427
<223> 99-15252-404.probe

<220>
<221> primer_bind
<222> 385..403

<223> 99-15252-404.mis

<220>
<221> primer_bind
<222> 405..423
<223> 99-15252-404.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15252.pu

<220>
<221> primer_bind
<222> 433..452
<223> 99-15252.rp complement

<400> 52
atgggggcat atagcaaccc tttagaaaca aaactacaaa aggtaagctt gtcttcttgc 60
atttcctttc tcttactaca tttaacatgg gaggttttct atgtctcaca ttcaaatatt 120
ctcactcggg ctgcctaatt tttccctgat tttccatcac tctttatgaa ggcttgctac 180
tttagaatac acatttttctt aacagaagat aataatcaga agatgtctcc caaatataag 240
tccaaatctt tcctatcatg ctgtgttctt tggctctttt gactttattt gaagtcagcc 300
ttgaagggga tagagatagg ctgtatgaag tccacgctga gaagttttgc cctgccctac 360
ttgtcctgta atatttcatg gatagcccag tggtgattaa accygtgtgt acaggaataa 420
ccatgagaat ttgttaaaaa tataggctct gg 452

<210> 53
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 382
<223> 99-15253-382 : polymorphic base C or T

<220>
<221> misc_binding
<222> 359..405
<223> 99-15253-382.probe

<220>
<221> primer_bind
<222> 363..381
<223> 99-15253-382.mis

<220>
<221> primer_bind
<222> 383..401
<223> 99-15253-382.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15253.pu

<220>

<221> primer_bind
<222> 459..477
<223> 99-15253.rp complement

<400> 53
aaaatcaatt ccccaacact cattttgtac gctaattttg taagatcctg aaaagtttca 60
ctatttttatg gtttcatgtg ttacagatga aaaaaaaact agaattcaaa ttttctgagt 120
tttttttttac aatattttat gattacaaag ttagaagact aagaataaaa tggcctaatt 180
tccataatgt gagtggtaaa tgcagagcac tggcctaaag aaaatatttc aaaaaattag 240
tcatcttttc cttaattttt ttccaaccta tgatctgttg aatgagcatt ttgcatatat 300
aaataaataa attactttgt aaataatctt gactggtttc tgttgaccac agtaacccac 360
tgcacagcac agcctgtaat tyctatgaac ctagggaaat gtatttaagt ttatttttg 420
attacacagg tcctcattgt gtaactaaac attgcataga atatgccagt gatgatg 477

<210> 54
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 392
<223> 99-15256-392 : polymorphic base C or T

<220>
<221> misc_binding
<222> 369..415
<223> 99-15256-392.probe

<220>
<221> primer_bind
<222> 373..391
<223> 99-15256-392.mis

<220>
<221> primer_bind
<222> 393..411
<223> 99-15256-392.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15256.pu

<220>
<221> primer_bind
<222> 439..456
<223> 99-15256.rp complement

<400> 54
cctctctatg atgcttccta ttaagcaatt ggggaaatgt aataaacaag ggttggtgag 60
catcttcctt agtgagatgt ttttggaaga attggataat tgagtgaata atagtgagaa 120
actcctgtgt ctgatgttgc tccatgttgg aatgctttta tgttctcaga gaatgagtca 180
ctgagagcca attgtgatga tacacaatgg ttttacccag gttggatatg gtcctctgta 240
ctggtaccct ttaagtcagt ggcactaatc agtcagtcat tgtcatgctt tgtgttggtc 300
catcatatgg tatgccctct tagagaacat cctgattagt ccttagacat cttttcaatt 360
tgaacactgg ggctcctcat tcgggtaaaa aytatggaca gtcagtgaaa ctgttgcaat 420
ggcccctcat agcagattgg atctcaatgc actttg 456

<210> 55
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 200
<223> 99-15261-202 : polymorphic base A or G

<220>
<221> misc_binding
<222> 177..223
<223> 99-15261-202.probe

<220>
<221> primer_bind
<222> 181..199
<223> 99-15261-202.mis

<220>
<221> primer_bind
<222> 201..219
<223> 99-15261-202.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15261.pu

<220>
<221> primer_bind
<222> 481..501
<223> 99-15261.rp complement

<400> 55
cttctaatcc tttgtttcca cttatttttat ttcattcctc attttatccc ttttttctaa 60
attccatttt attatactta aggtgctttt aatatggtta tcatactcct gatagtgtta 120
tttcttttctt agtcttctta tataagcgct atacgttcac attccatctc ctttggttat 180
ctttccattt cttcaccgar cctctttgct ctctttttt atagctggtt cactcaaaat 240
gtcttacttt gccatttttg aaatttattt tcattctttt atgtactgaa taaaatttaa 300
aaatacttta tcatggtggg aggtacccgt gatgtccaaa taagtgttta tattaattgt 360
tggggttttt ttgtttgtgt gttttttgaa aggttaagaa aatctcattc agaaagtaag 420
ttgtttaaaa attctggacc aaatttacca cacatcaagc agatacttac caagttgttt 480
ggtagacatt agcagtattt a 501

<210> 56
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 432
<223> 99-15280-432 : polymorphic base C or T

<220>

<221> misc_binding
<222> 409..455
<223> 99-15280-432.probe

<220>
<221> primer_bind
<222> 413..431
<223> 99-15280-432.mis

<220>
<221> primer_bind
<222> 433..451
<223> 99-15280-432.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15280.pu

<220>
<221> primer_bind
<222> 521..541
<223> 99-15280.rp complement

<400> 56
atgtccatcc atcttgccca gagagagttt ctacaacact tcctctgcaa gccctttccc 60
tacttgcctc acctattgct ttcctctgtt acgttgtatt cccctcactg tttcttccaa 120
catcttccca cctcagagca tggacacttg ctgctctttc tgtgtcatga tgctgctcac 180
ttgtcccttt cttaatgtct cctccctgag ccaatcttct ccacccccac aacttacgca 240
cacttacatg tcatattttc cttcatagcc tttaacacca tttgaaatga tatatatttg 300
attgctttta aaatttctct gtccccccac taaatataaa cttcaggatg gcaagaatgt 360
agtccattat cttatttctc cagcctccat acttttaaga aaataaattt tggttgtata 420
agccatccag tyagtggtac ttggttatag caccctagc aaaagaatac aaaaaaaggg 480
agaatgtttg caatcatctg tttgaggcta ggaattccca gagagggaaa caaggagtaa 540
t 541

<210> 57
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 428
<223> 99-15353-428 : polymorphic base C or T

<220>
<221> misc_binding
<222> 405..451
<223> 99-15353-428.probe

<220>
<221> primer_bind
<222> 409..427
<223> 99-15353-428.mis

<220>
<221> primer_bind

<222> 429..447
<223> 99-15353-428.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15353.pu

<220>
<221> primer_bind
<222> 495..514
<223> 99-15353.rp complement

<400> 57
tgggaatgga ggtagtagac gatgaggtct ccaccctctg actttgcaga gatgggcaag 60
gccaagtgtt ggaagggctt aaacacacac cggagtattc tgtgagaacc agtggatttc 120
agaggatggc aatgacacca cttgccttct gcctcaggag gataactgat ggccgtgtgt 180
gggatgcact ggagagcaag agctggcttg cagggagacc agctggatga ttttctttca 240
tttatttttat tcattcaaca cacattcatc tggggttcac tctgtgccca acactgggca 300
tttccaaata gtccagatgg cagtaagcat ggttgtggca gtaggaatgg gaaggctggg 360
aggggtatga gaggcattac aaacgggaag tgggagtggc accccagaaa agtctagttt 420
aaggtgcyag tggatgtgtg catgtgtgcg cgggggtgtc tagagggtgg cgggcagctg 480
gaaattgagg tcaagtgctt aaagaacaac tcgt 514

<210> 58
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 150
<223> 99-15355-150 : polymorphic base C or T

<220>
<221> misc_binding
<222> 127..173
<223> 99-15355-150.probe

<220>
<221> primer_bind
<222> 131..149
<223> 99-15355-150.mis

<220>
<221> primer_bind
<222> 151..169
<223> 99-15355-150.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15355.pu

<220>
<221> primer_bind
<222> 471..489
<223> 99-15355.rp complement

<400> 58
taacttctcc gtctctcctt cttagcccat atgtcaataa tgactgaaag tattcatttc 60
catctttaaa ctgcctattc cagccacctc ccacctccat ctctttcctt ctaagttttc 120
ttcatcttct actttgggca aaaggaaaty gatgtgtcag acaggcctag ttttgaattc 180
tggatctgct agcacttctc tgtgtgtcct tggttatatg atatagtctt aaaccttaat 240
gttcttgcct gtaaaatggg gataataaaa acctcttaac agtggttgtt tcatgcagct 300
ttcattacaa acttcctcat tcaaaatctt caatgatttc cattttcac aaaatgaaat 360
tcaaaatttc tgtagattat tgagacaagt cccctactct tcacctaaat ttatctttta 420
tttattctct catcattatc aacaactact aggctttgtt gccttgactc cagaggcaaa 480
aatcttatc 489

<210> 59
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 227
<223> 99-15685-227 : polymorphic base A or G

<220>
<221> misc_binding
<222> 204..250
<223> 99-15685-227.probe

<220>
<221> primer_bind
<222> 208..226
<223> 99-15685-227.mis

<220>
<221> primer_bind
<222> 228..246
<223> 99-15685-227.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15685.pu

<220>
<221> primer_bind
<222> 449..468
<223> 99-15685.rp complement

<400> 59
aaacaaaggc acgcagagga taaggcatga gtccaaccag cagcatctcc ctcccgaatg 60
agtacagaaa tgatcaatac tcgaagagaa aaagatgctt tcagtgtgct ttacctgaaa 120
acttccttaa gcagcttcac tttattgtca ggatatcgct ttgtgtttgt atcatctaag 180
aaagctcgcg catatgctag tgggccagca ttgacctaga caaagarcaa agattttcag 240
ttccactagg aagaaaatca ccatgaccat ctgctcagtt tcagtttgca ggcactaaaa 300
agcccgttcg cgtgagctac tcacaatccc tgccttccag gaacttaagc ccaaaaagaa 360
accacaaagc tcactctgtt gcacaccact tgattccatg atctcagcca tcttcagggc 420
acttgtgatg atggtttact ttatgtaaga agaaaccaat gcttggaa 468

<210> 60

<211> 500
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 428
<223> 99-15695-428 : polymorphic base C or T

<220>
<221> misc_binding
<222> 405..451
<223> 99-15695-428.probe

<220>
<221> primer_bind
<222> 409..427
<223> 99-15695-428.mis

<220>
<221> primer_bind
<222> 429..447
<223> 99-15695-428.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15695.pu

<220>
<221> primer_bind
<222> 481..500
<223> 99-15695.rp complement

<400> 60
atcagccttt gtgaggagga ggccctgcct gctctcctcc tgagctgatg ggtcagtcac 60
accaggacaa aggtctgccc ggggctgtgt gggttcctcc ttcctgagct gcacaccagc 120
atctgctgaa caccttctgg agctcagctc agtgtctcgt ccagagacac tggttccctt 180
ggcttctcag caactctcgg atctgggcct gggtctaacc tcagcggtgg tcttgcccat 240
ttctagggcc tcacaattca gcctcatgtc ttcacctgtg gctcttttgc aaggctcaga 300
aagctctagg gtcagttcca gatgactccc accagcatgc cagtaggagc caccaccccc 360
tctcagccag cgccaccata ttccaggcaa attccaactg acacagactt caaggaacga 420
ttgtagcygt tgttcttgct tcttccaaat ggaagagtgc attattgggg tcccttctag 480
cacgcatttc attccccacc 500

<210> 61
<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 310
<223> 99-15703-310 : polymorphic base C or T

<220>
<221> misc_binding
<222> 287..333

<223> 99-15703-310.probe

<220>
<221> primer_bind
<222> 291..309
<223> 99-15703-310.mis

<220>
<221> primer_bind
<222> 311..329
<223> 99-15703-310.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15703.pu

<220>
<221> primer_bind
<222> 452..472
<223> 99-15703.rp complement

<400> 61
agggctttgg gttataggcg ctgaatttct tctaaagcta acctgactct gatgctagaa 60
gagcccattt aaggaaagaa aaacactttt cattgctcga tcaaagttca tccattttgg 120
aaaagacatc aaaccaagtg tgtgacacca ggcacccata tccttcctct ttcccaccac 180
cccacccctg tcctcagggc agtgacagtg aagcctggtg caggtcccgc tgctgctttt 240
tgaagtggca catgctttat tttcttaaaa agaagtgaga gacaacctat gctacaggag 300
gctctgtgay gtttttctga agtacaaccc cttgctctgc cagggcagct gtaaagggtc 360
taaagagccc tgagaaagga gagaggattt gggaagccga ggaggcagag ggagaccaca 420
tagcacatgg agttctgaaa gggcccaagt ggagacagaa aacgagtcat gt 472

<210> 62
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 400
<223> 99-15870-400 : polymorphic base A or G

<220>
<221> misc_binding
<222> 377..423
<223> 99-15870-400.probe

<220>
<221> primer_bind
<222> 381..399
<223> 99-15870-400.mis

<220>
<221> primer_bind
<222> 401..419
<223> 99-15870-400.mis complement

<220>

<221> primer_bind
<222> 1..21
<223> 99-15870.pu

<220>
<221> primer_bind
<222> 452..470
<223> 99-15870.rp complement

<400> 62
gctcaaatgt atcaaacaca gtttctgtgg tcaagttcct ctccttttct aaatttgctt 60
agaggatctc ataaaacgta actcctctga caagggaacc attttagcac caacactgca 120
aaagcttctg tgttcctaag ggaaagatcc tttcctgaat taaatttaac ctctttagta 180
ctcccattta gccacctgat aaatccactt gagctatctt ttgggaagag agaggtatct 240
gggaacaata acacttcctt tttgaacagt ttaataaagc tttgtgagat ttcaagatga 300
aagataatgt gtaatgctga tagtgccctc caaggctctg cattcatgga tccaattacg 360
ttttttgtca tggtaaaagc cacagtggat atattaaatr agagtgtggt ttaagaatga 420
aggcccagga gtctggagat ctggtttcta aggctgactt cacttctgct 470

<210> 63
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 287
<223> 99-16321-287 : polymorphic base A or C

<220>
<221> misc_binding
<222> 264..310
<223> 99-16321-287.probe

<220>
<221> primer_bind
<222> 268..286
<223> 99-16321-287.mis

<220>
<221> primer_bind
<222> 288..306
<223> 99-16321-287.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-16321.pu

<220>
<221> primer_bind
<222> 451..469
<223> 99-16321.rp complement

<400> 63
ctttaggaat atcccttctg atttgaacaa cattttgcta tccaagttct gtctactttt 60
ttaacaagtt cttgctccgt gtgtctcctt ttgcttgttc tcaagtaagg gagtaacagg 120
gataaactcc cactccttgg taaatctttc tatcattttt ggaaatctca tccattgtag 180

taaatgctct taaatcttca tcttcaggcc gtgacttcca tctagcctcc attcacgttt 240
ccgggtttat gtctgcaatg agcattccgt ggctctacat agatgcmcca ccatacctag 300
aacccatgta tcccaaactc aattctttct ttcccaggac attacttcct gcacttcctt 360
agtctatcaa tggcactgtt attctcttga ccatctagac ttgaaatttt ggggtttgga 420
ctcctcctgc tcccttgctt tatatgtaat cagacatcaa gtctcaatc 469

<210> 64
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 194
<223> 99-16333-194 : polymorphic base A or G

<220>
<221> misc_binding
<222> 171..217
<223> 99-16333-194.probe

<220>
<221> primer_bind
<222> 175..193
<223> 99-16333-194.mis

<220>
<221> primer_bind
<222> 195..213
<223> 99-16333-194.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16333.pu

<220>
<221> primer_bind
<222> 524..544
<223> 99-16333.rp complement

<400> 64
atttaccccg tctgccttgc aatttcagga tcagtataca tcaaatcaag tgaacaaccc 60
agggaattct gccgttacct tttagaaaca gaataaatat taacagagct ttacttcttt 120
ccaccaagga ggactatatg ttaatacagt aatttacact ggaaaaaata taaatgaaag 180
ggtttagaac ctcrtaactt taaaaataac ataattcctc ctagaacatt cctttcactt 240
gtgattctca aagcactttg catttcccag ctattggcag ggctggaatt aggatcaaag 300
tatcactaaa tggtaggtga aataaatgtg aagctgattt tcaggagtac aggaatggag 360
tcatcaggcg actttaaagt taagaatctg ttggagcagc tgccaataaa tcaaggccca 420
aaggagaaag ttctttggaa accttgaaat attgtataca tttagataat tattgttgtt 480
gtcaatgtta acgaaaaaag caataaatca gggagatggc actgatgagt gaggagaaat 540
agac 544

<210> 65
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 149
<223> 99-5873-159 : polymorphic base C or T

<220>
<221> misc_binding
<222> 126..172
<223> 99-5873-159.probe

<220>
<221> primer_bind
<222> 130..148
<223> 99-5873-159.mis

<220>
<221> primer_bind
<222> 150..168
<223> 99-5873-159.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-5873.pu

<220>
<221> primer_bind
<222> 457..475
<223> 99-5873.rp complement

<220>
<221> misc_feature
<222> 409
<223> n=a, g, c or t

<400> 65
gcgtaacaat aagcagggtt agtcgccaca aaacttgaga taagaggaaa actaaaaaag 60
tctaatgaaa tcagtagtct taaaaagatg acatgatagg aagagaagtg ttaaaaaaga 120
aaaaaaatag gtatgaaaga gagtaacaya taccggaaaa gggataaaat acatcctttg 180
aaagaacaaa gagttattca aattgaattc ttaatgaatt acttaaacag cagattagat 240
attgttaaaa agaggaatag ggaattaaat gatatatgtg atgatattac ctagtgtaac 300
catcaaagat gtattgcaaa tgataaagaa aaaaatgctg ccatggcaat attaatatca 360
taaaaatata ctttaagaag taaataaatg caactaggaa tagagaaans dvhatgaata 420
ataatattta amaaavvgta taacaagtat acataagatg taatatccta aaccg 475

<210> 66
<211> 511
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 49
<223> 99-5912-49 : polymorphic base A or G

<220>
<221> misc_binding
<222> 26..72

<223> 99-5912-49.probe

<220>
<221> primer_bind
<222> 30..48
<223> 99-5912-49.mis

<220>
<221> primer_bind
<222> 50..68
<223> 99-5912-49.mis complement

<220>
<221> primer_bind
<222> 11..31
<223> 99-5912.pu

<220>
<221> primer_bind
<222> 494..511
<223> 99-5912.rp complement

<400> 66
aaatataata gtcaaatcat gttaccatta ggacacatta aaaatgtcra attaccttgg 60
gaccttatat gaacatatta agataataat gatagtgttc agtgcaatat tcagatcaat 120
agtttaaacc caaaatattt ataccttcag attagatgta tgcaaatgca ttgattcatg 180
tgtcttttat ctgttgttta catttggaga aatatttgag aaatatttca aaatggaatt 240
tatataaatt taaacacata atggttttat gtaaaaatat tgctaaatta cattttcccc 300
ttaattctta tttcttggaa acgtgcctta gtcgctgaaa tattcataca ttaacacaat 360
gaaagaagtg aaccttacta ggctttgact atcaggtttg ctgttggttt ttgactattg 420
tgaaactata gcctgatttc taaatcagga agaaacgtgt attgttgtta atatggacac 480
atgacatatt tgtctgcctg acttttgatc c 511

<210> 67
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 210
<223> 99-6012-220 : polymorphic base G or T

<220>
<221> misc_binding
<222> 187..233
<223> 99-6012-220.probe

<220>
<221> primer_bind
<222> 191..209
<223> 99-6012-220.mis

<220>
<221> primer_bind
<222> 211..229
<223> 99-6012-220.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-6012.pu

<220>
<221> primer_bind
<222> 467..485
<223> 99-6012.rp complement

<400> 67
gtcttgactt gttttcctga gggtccaggt tgatttgcat gctcttgagg aaatatacac 60
gtcttctcag ttttaataat tgactgacag ccctgtggtt tctcaggacc cagtgagctg 120
ctgctcccag gtcagtctgc aaaggatgct ggttcccttg tggtctcatc aaggtgagga 180
atttcctgat tttagagatt tctttatcck aattttgaag actttctttc acatttctag 240
gcataaaaaa atgtacagca ctctactgct tgtttaacaa atggatagtg atatatctgc 300
caacaaagac cacatggagt atttcattga ctatcagaga agtttcctcg aaaggcacca 360
tacttagtgt tttatttcca tgagtgaagg aaaattagtt atttgaagta tttggctgtc 420
tttagttgtt tctaaagtag tgctgatttt atatgcccat aatattcata tatacaccca 480
ggata 485

<210> 68
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 89
<223> 99-6080-99 : polymorphic base C or T

<220>
<221> misc_binding
<222> 66..112
<223> 99-6080-99.probe

<220>
<221> primer_bind
<222> 70..88
<223> 99-6080-99.mis

<220>
<221> primer_bind
<222> 90..108
<223> 99-6080-99.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-6080.pu

<220>
<221> primer_bind
<222> 509..529
<223> 99-6080.rp complement

<400> 68
aaatgtgtcc ctgaaaccca tgctatattc aactgaatat tctaatgtct ttgattacaa 60

agccatctct agcaatttaa tacaattayg aaatggaaaa gttggcaaat gcaaaacaat 120
agctcgtgtt caaggtatgt ctttattagg ggaagtttat cgaaacagat gtttatgcta 180
tttcctataa actagattct aaaatatttt attctataaa gatgtattga ctttatatga 240
aaaaattatt gaaaaatcta caagatggtg aaactcttta gaactatatt tctattacaa 300
gtttatttt aatttcaaaa atgtactgca taaatgcagc aaaaccttta ttgtcacata 360
ttaaaacatg tacattattg tgtgcaaatt aaaatttcat taccttaaac caaaaagtga 420
gttggccaga tagtaaataa tttaggctct aaggctgaaa agcgcttgta ttaattactc 480
aactccacca ctattttgcc aaagcagtca cagacaatac gcattcaca 529

<210> 69
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 156
<223> 99-7308-157 : polymorphic base C or T

<220>
<221> misc_binding
<222> 133..179
<223> 99-7308-157.probe

<220>
<221> primer_bind
<222> 137..155
<223> 99-7308-157.mis

<220>
<221> primer_bind
<222> 157..175
<223> 99-7308-157.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-7308.pu

<220>
<221> primer_bind
<222> 469..489
<223> 99-7308.rp complement

<400> 69
tgtggtctgg atatggtgra ctgtccttca cacacagatg tgggaagcca tgatcatcag 60
ttgcattatt cctgaggggc aatgcattcc agttacatag aaccagtttc tacgtttcag 120
ggtatatgta ttcatggtga caaatttatt cacatyttaa gtaattttaa gtaattcaca 180
ttttaagtaa ttttcctgaa tgtgcctcat tggcttctgt gcctcttcag aaaagatgaa 240
ctaaacactg gcatatgtgt tcagatttca acattccgtt gttttcattg tggataattt 300
ctgtcccata tttttgtgta aagttagaca ataaagtgtt aatattctgg cgtcggcaca 360
ttttctttcc tgataaataa caattcacat atctttttaa aatatcagag aatatagtaa 420
ccaatttcca attctttttt caccatgtat ctattggagt tttaaaatga ctaatactaa 480
ggcaactat 489

<210> 70
<211> 18
<212> DNA

<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerPU

<400> 70
tgtaaaacga cggccagt 18

<210> 71
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerRP

<400> 71
caggaaacag ctatgacc 18